

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 12:56:17 ; Search time 23 Seconds

(without alignments)
484.580 Million cell updates/sec

Title: US-09-862-802-2
Sequence: 1 MTSEITYAEVRFKNEKSSG.....NDVNCIGPQRVCENMKIHL 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	251	19.6	301	1	LEC1_MOUSE
2	232	18.1	301	1	LEC1_RAT
3	228.5	17.9	283	1	LEC1_RAT
4	227.5	17.8	306	1	MMGL_RAT
5	224	17.5	207	1	LEC1_CHICK
6	223.5	17.5	311	1	LEC1_HUMAN
7	220.5	17.2	290	1	LEC1_HUMAN
8	218	17.0	283	1	LEC1_HUMAN
9	216.5	16.9	304	1	LEC1_MOUSE
10	213	16.6	348	1	MMGL_MOUSE
11	208.5	16.3	331	1	FCCE2_MOUSE
12	196	15.3	550	1	KUCR_RAT
13	187	14.6	1268	1	PGCN_MOUSE
14	184	14.4	1257	1	PGCN_RAT
15	184	14.4	1321	1	PGCN_HUMAN
16	183.5	14.3	2124	1	PGCA_RAT
17	181	14.1	2364	1	PGCA_BOVIN
18	176	13.8	2109	1	PGCA_CHICK
19	176	13.8	2132	1	PGCA_MOUSE
20	176	13.8	2415	1	PGCA_HUMAN
21	175.5	13.7	155	1	PLC_HALLA
22	175.5	13.7	220	1	NK1D_MOUSE
23	175	13.7	216	1	NKGD_MACMU
24	175	13.7	2333	1	PGCA_CANFA
25	174	13.6	173	1	LIT2_MOUSE
26	171.5	13.4	1456	1	MANR_HUMAN
27	170	13.4	266	1	KLR3_MOUSE
28	170	13.3	223	1	NK12_MOUSE
29	168	13.1	173	1	LEC2_MEGRO
30	168	13.1	883	1	PGCB_MOUSE
31	168	13.1	3562	1	PGCV_CHICK
32	167	13.0	163	1	ANP_HUMAN
33	167	13.0	216	1	NKGD_HUMAN

34	167	13.0	912	1	PGCB_BOVIN	Q28062	bos taurus
35	165.5	12.9	321	1	FCCE2_HUMAN	P06734	homo sapien
36	165	12.9	883	1	PGCB_RAT	P5068	rattus norv
37	164	12.8	223	1	NK13_RAT	P27471	rattus norv
38	162.5	12.7	227	1	NK11_MOUSE	P27811	mus musculus
39	159.5	12.5	162	1	LEC3_MEGRO	P07439	megabalanus
40	158	12.3	233	1	NKGA_MACMU	Q9m23	macaca mula
41	157.5	12.3	179	1	CD94_MACMU	Q9m2K9	macaca mula
42	155	12.1	165	1	LIT1_MOUSE	P43137	mus musculus
43	155	12.1	266	1	KLR5_MOUSE	Q60652	mus musculus
44	154	12.0	179	1	CD94_HUMAN	O13241	homo sapien
45	154	12.0	2738	1	PGCV_RAT	O9erb4	rattus norv

ALIGNMENTS

```

RESULT 1
LECI_MOUSE          STANDARD;          PRT;          301 AA.
ID LECI_MOUSE
AC P24721:
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)
DE (ASGP-R).
GN ASGR2 OR ASGR-2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91027942; PubMed=223888;
RA Sanford J.P., Doyle D.;
RT "Mouse asialoglycoprotein receptor cDNA sequence: conservation of
RT receptor genes during mammalian evolution.";
RL Biochim. Biophys. Acta 1087:259-261(1990).
CC -1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
CC WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX
CC CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES
CC TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND
CC BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
CC TRANSLOCATED TO A SORTING ORGANELLE WHERE RECEPTOR AND LIGAND ARE
CC DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
CC SURFACE.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
CC CELLS.
CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL: X53042; CAA37211.1; -
DR PIR: S13165; S13165.
DR HSSP: P06734; HHLI.
DR MGD: MGI:88082; Asgr2.
DR InterPro: IPR002353; Antifreeze2.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR005640; lectin_N.
DR Pfam: PF00059; lectin_C_1.
DR Pfam: PF00954; lectin_N_1.
DR PRINTS: PR00356; ANTIFREEZE2.1.
DR SMART: SM00034; CLCCT; 1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.

```

	DR	PROSITE; PS50041; C-TYPE LECTIN-2; 1.
	KW	Lectin; glycoprotein; Receptor; Endocytosis; Transmembrane;
	FT	Calcium; Signal-anchor; Phosphorylation
	ET	DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
	FT	TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
	FT	(POTENTIAL).
	FT	DOMAIN 80 301 EXTRACELLULAR (POTENTIAL).
	FT	DISULFID 169 295 C-TYPE LECTIN (LONG FORM).
	FT	DISULFID 170 181 BY SIMILARITY.
	FT	DISULFID 198 293 BY SIMILARITY.
	FT	DISULFID 271 285 BY SIMILARITY.
	FT	CARBONYD 97 97 N-LINKED (GLCNAG. .) (POTENTIAL).
	FT	CARBONHD 165 165 N-LINKED (GLCNAG. .) (POTENTIAL).
	FT	CARBONDH 298 298 N-LINKED (GLCNAG. .) (POTENTIAL).
	SQ	SEQUENCE 301 AA; 34907 MW; 3A29FAIABA6BF298 CRC64;
	Query Match	19.6%; Score 251; DB 1; Length 301;
	Best Local Similarity	25.2%; Pred. No. 1.5e-14;
	Hatches	65; Conservative 38; Mismatches 75; Indels 80; Gaps 7
Df	42	PFKLLCAALLFFLFLAISFIATFY-----PFQKYS-----73
Oy	49	FPRRCSCSFRLSLALANILLIVICVSSOSIOLOBEFRKRKFESFSSTLMGEA 108
Dd	74	-----QLKKTKTVELVHTLECYNKNMPY-----EETAMS 104
Oy	109	LDTLGGSTNALITLSMALOLEEKOOKADHSHTLLFHLPFPMDLTLCOLAFGSGNTE 168
Oy	105	CCPKWKCFSSNCYFIITESASWOSEDKARMHAHLVIYMFOEPDFIFONTLESAVF 164
Dd	169	CCPNWMVEFGSCTWFERSDGLTMAVDYCYLENHNLIIINSREDDVVAKH-KSQPHIM 227
Oy	165	VGLSDPEGRHMQUAVDOTPYVESSTFWHPREPSPDNERNCYLVNFPSRKRMG-----216
Dd	228	I GLTDROGS--WKWDVGDIYSNYENNAFTPDP-----NMHGHEQGEGDECATILLS 276
Oy	217	--WNADVCLGPORSYCE 231
Dd	277	DGHMNDNFQQOVNRWC E 294
RESULT 2		
ID	LECT_RAT	STANDARD:
AC	P08290:	PRT: 301 AA.
Dt	01-AUG-1988	(Rel. 08, Created)
Oc	01-NOV-1990	(Rel. 16, Last sequence update)
Dd	30-MAY-2000	(Rel. 39, Last annotation update)
De	Asialoglycoprotein receptor R2/3	(Hepatic lectin 2/3) (RHL-2) (ASGP-R) (ASGP.R).
Gn	ASGR2 OR ASGR-2.	
Os	Rattus norvegicus (Rat).	
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Oc	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
Xx	NCB1_taxid=10116;	
Rn	[1]	
Rp	SEQUENCE FROM N.A.	
Rk	MEDLINE=87257885; PubMed=3600647;	
Ra	McPhaul M., Berg P.;	
Rt	"Identification and characterization of cDNA clones encoding two homologous proteins that are part of the asialoglycoprotein receptor";	
Rl	Mol. Cell. Biol. 7:1841-1847(1987);	
Rn	[2]	
Rp	SEQUENCE FROM N.A.	
Rk	MEDLINE=87250656; Pubmed=3597443;	
Ra	Halberg D.F., Wager R.E., Fairrell D.C., Hildreth J., Quesenberry M.S., Loeb J.A., Holland E.C., Drickamer K.;	
Rt	"Major and minor forms of the rat liver asialoglycoprotein receptor are independent galactose-binding proteins. Primary structure and glycosylation heterogeneity of minor receptor forms.";	
Rl	J. Biol. Chem. 262:9828-9838(1987);	
Rn	[3]	

Query Match	Best Local Similarity	Score	DB 1:	Length	DB 2:	Score	DB 3:	Length
SEQUENCE FROM N.A.	18.1%	232	DB 1:	301	SEQUENCE FROM N.A.	18.1%	232	301
STRAIN-Sprague-Dawley; TISSUE-Liver;	25.6%	13	DB 2:	13	STRAIN-Sprague-Dawley; TISSUE-Liver;	25.6%	13	13
MEDLINE-89170119; PubMed-3234178;			DB 3:		MEDLINE-89170119; PubMed-3234178;			
Sanford J.P., Elliott R.W., Doyle D.;					Sanford J.P., Elliott R.W., Doyle D.;			
"Asialoglycoprotein receptor genes are linked on chromosome 11 in the					"Asialoglycoprotein receptor genes are linked on chromosome 11 in the			
mouse.";					mouse.";			
DNA 7:721-728(1988).					DNA 7:721-728(1988).			
[4]					[4]			
SEQUENCE OF 201-301.					SEQUENCE OF 201-301.			
MEDLINE-84111554; PubMed-6319386;					MEDLINE-84111554; PubMed-6319386;			
Dieckmeyer K., Mamou J.F., Bins G., Leung J.O.;					Dieckmeyer K., Mamou J.F., Bins G., Leung J.O.;			
"Primary structure of the rat liver asialoglycoprotein receptor.					"Primary structure of the rat liver asialoglycoprotein receptor.			
Structural evidence for multiple polypeptide species.";					Structural evidence for multiple polypeptide species.";			
J. Biol. Chem. 259:770-778(1984).					J. Biol. Chem. 259:770-778(1984).			
-1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO					-1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO			
WHICH THE TERMINAL SIALIC ACID RESIDE ON THEIR COMPLEX					WHICH THE TERMINAL SIALIC ACID RESIDE ON THEIR COMPLEX			
CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES					CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES			
TERMINAL GALACTOSE AND N-ACETYLGLUCOSAMINE UNITS. AFTER LIGAND					TERMINAL GALACTOSE AND N-ACETYLGLUCOSAMINE UNITS. AFTER LIGAND			
BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND					BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND			
TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE					TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE			
DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE					DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE			
SOURCE.					SOURCE.			
-1- SUBCELLULAR LOCATION: Type II membrane protein.					-1- SUBCELLULAR LOCATION: Type II membrane protein.			
-1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL					-1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL			
CELLS.					CELLS.			
-1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.					-1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.			
-1- MISCELLANEOUS: TWO TYPES OF RAT HEPATIC LECTIN HAVE BEEN					-1- MISCELLANEOUS: TWO TYPES OF RAT HEPATIC LECTIN HAVE BEEN			
IDENTIFIED, RHL-1 AND RHL-2/3, HAVING A RELATIVE ABUNDANCE OF 4:1.					IDENTIFIED, RHL-1 AND RHL-2/3, HAVING A RELATIVE ABUNDANCE OF 4:1.			
RHL-2 AND RHL-3 ONLY DIFFERS IN THEIR CARBOHYDRATE STRUCTURES.					RHL-2 AND RHL-3 ONLY DIFFERS IN THEIR CARBOHYDRATE STRUCTURES.			
-1- SIMILARITY: Contains 1 C-type lectin family domain.					-1- SIMILARITY: Contains 1 C-type lectin family domain.			
-----					-----			
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or send an email to license@isb-sib.ch).					or send an email to license@isb-sib.ch).			
-----					-----			
DR EMBL; M16347; AAA42038.1; -					DR EMBL; M16347; AAA42038.1; -			
DR EMBL; J02762; AAA41522.1; -					DR EMBL; J02762; AAA41522.1; -			
DR EMBL; X07636; CAA30476.1; -					DR EMBL; X07636; CAA30476.1; -			
PIR; B28462; LNR2.					PIR; B28462; LNR2.			
HSSP; P06734; 1HI1.					HSSP; P06734; 1HI1.			
InterPro; IPR002353; AntifreezeZell.					InterPro; IPR002353; AntifreezeZell.			
DR InterPro; IPR001304; Lectin_C.					DR InterPro; IPR001304; Lectin_C.			
InterPro; IPR005640; Lectin_N.					InterPro; IPR005640; Lectin_N.			
Pfam; PF00059; lectin.C.1.					Pfam; PF00059; lectin.C.1.			
Pfam; PF03954; lectin.N.1.					Pfam; PF03954; lectin.N.1.			
PRINTS; PR00356; ANTIFREEZE2II.					PRINTS; PR00356; ANTIFREEZE2II.			
SMART; SM00034; CLECT; 1.					SMART; SM00034; CLECT; 1.			
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.					DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.			
DR PROSITE; PS00041; C-T								

DE galactose/N-acetylglucosamine-specific lectin) (MGL).
 GN MGL OR MGL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=90293078; PubMed=2358462;
 RA Ii M., Kurata H., Itoh N., Yamashina I., Kawasaki T.;
 RT "Molecular cloning and sequence analysis of cDNA encoding the
 RT macrophage lectin specific for galactose and N-acetylglucosamine."
 RL J. Biol. Chem. 265:11295-11298(1990).
 RN
 RP PRELIMINARY SEQUENCE OF 9-28.
 RX MEDLINE=88339956; PubMed=3421964;
 RA Ii M., Kawasaki T., Yamashina I.;
 RT "Structural similarity between the macrophage lectin specific for
 RT galactose/N-acetylglucosamine and the hepatic asialoglycoprotein
 RT binding protein."
 RL Biochem. Biophys. Res. Commun. 155:720-725(1988).
 CC
 CC -1- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE
 CC UNITS.
 CC -1- SUBUNIT: HOMO-OLIGOMER.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC
 CC EMBL: J05495; AAA41216.1; -
 CC PIR: A42230; A42230.
 DR HSSP: P06734; 1HLT.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR005640; Lectin_N.
 DR Pfam: PF00059; Lectin_C; 1.
 DR Pfam: PF03954; Lectin_C; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE: PS0041; C_TYPE_LECTIN_2; 1.
 DR PROSITE: PS0041; C_TYPE_LECTIN_2; 1.
 DR Lectin; Glycoprotein; Transmembrane; Calcium; Signal-anchor.
 DR DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
 DR TRANSMEM 38 58 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 DR (POTENTIAL).
 DR DOMAIN 59 306 EXTRACELLULAR (POTENTIAL).
 DR DOMAIN 174 300 C-TYPE LECTIN (LONG FORM).
 DR DISULFID 175 186 BY SIMILARITY.
 DR DISULFID 203 298 BY SIMILARITY.
 DR DISULFID 276 290 BY SIMILARITY.
 DR CARBOHYD 76 76 N-LINKED (GLCNAC...) (POTENTIAL).
 DR CARBOHYD 168 168 N-LINKED (GLCNAC...) (POTENTIAL).
 DR SEQUENCE 306 AA: 34242 MW: D68A5DF0B9BF13 CRC64;
 SO
 Query Match 17.8%; Score 227.5; DB 1; Length 306;
 Best local similarity 31.6%; Pred. No. 1,6e-12;
 Matches 48; Conservative 27; Mismatches 62; Indels 15; Gaps 5;

RESULT 5
 LECH_CHICK
 ID LECH_CHICK STANDARD; PRT; 207 AA.
 AC P02707;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hepatic lectin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91268022; PubMed=2050668;
 RA Bezouska K., Crichton G.V., Rose J.M., Taylor M.E., Drickamer K.;
 RT "Evolutionary conservation of Intron position in a subfamily of genes
 RT encoding carbohydrate-recognition domains."
 RL J. Biol. Chem. 266:11604-11609(1991).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88186849; PubMed=3281941;
 RA Mellow T.E., Halberg D., Drickamer K.;
 RT "Endocytosis of N-acetylglucosamine-containing glycoproteins by rat
 RT fibroblasts expressing a single species of chicken liver glycoprotein
 RT receptor."
 RL J. Biol. Chem. 263:5468-5473(1988).
 RN
 RP SEQUENCE.
 RX MEDLINE=81215504; PubMed=7240175;
 RA Drickamer K.;
 RT "Complete amino acid sequence of a membrane receptor for
 RT glycoproteins. Sequence of the chicken hepatic lectin."
 RL J. Biol. Chem. 256:5827-5839(1981).
 CC
 CC -1- FUNCTION: HEPATIC LECTIN IS A MEMBRANE RECEPTOR PROTEIN THAT
 CC RECOGNIZES AND BINDS EXPOSED N-ACETYLGALACTOSAMINE MOIETIES OF
 CC PLASMA GLYCOPROTEINS, THUS MEDIATING THEIR CLEARANCE (FROM THE
 CC CIRCULATION) AND ENDOCYTOSIS.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- PTM: SOME OR ALL OF THE CYSTEINES ARE INVOLVED IN DISULFIDE BONDS.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC
 CC EMBL: M63230; AAA48814.1; -
 CC EMBL: M63225; AAA48814.1; JOINED.
 CC EMBL: M63226; AAA48814.1; JOINED.
 CC EMBL: M63227; AAA48814.1; JOINED.
 CC EMBL: M63228; AAA48814.1; JOINED.
 CC EMBL: M63229; AAA48814.1; JOINED.
 CC EMBL: M63229; AAA48814.1; JOINED.
 CC EMBL: J03188; AAA48937.1; -
 CC PIR: A03167; LNCNL.
 CC HSSP: P20693; 1HLT.
 CC InterPro: IPR001304; Lectin_C.
 CC Pfam: PF00059; Lectin_C; 1.
 CC SMART: SM00034; CLECT; 1.
 CC PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
 CC PROSITE: PS0041; C_TYPE_LECTIN_2; 1.
 CC Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
 CC Signal-anchor; Acetylation.
 CC MOD_RES 1 1 ACETYLATION.
 CC FT DOMAIN 1 23 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 24 48 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 FT

```

FT DOMAIN 49 207 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 77 203 C-TYPE LECTIN (LONG FORM).
FT DISULFID 78 92 BY SIMILARITY.
FT DISULFID 109 201 BY SIMILARITY.
FT DISULFID 179 193 BY SIMILARITY.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 207 AA; 24216 MW; 1F6B36FDB32899DB CRC64;

Query Match 17.58; Score 224; DB 1; Length 207;
Best Local Similarity 27.88; Pred. No. 2e-12;
Matches 54; Conservative 35; Mismatches 79; Indels 26; Gaps 7;

QY 49 SLIFPLLAISFEIAFV---IFFOKYSOLLEKTKTELVHTTLECKKNMPYEETWSC 105
DB 24 SFAAYVLLALSLFLLTLSSVSLARIALSSKLSITQ-----SEPKHNFSSDLSLFP 77
QY 106 C---PNMKSFSNCFYISTESASWDSKDCARMEAHLLVINTQEBDFPONTJESBA 162
DB 78 CGAQSROMEYFEGRCYFSLSRMSMHKAKACEEMSHLIIIDYAKONFVMPETRNE-R 136
QY 163 YFGLSDPREGQRHMOWDQTPYNESSTFMHPRESDP--NERCVVLFKRSKPRM---GW 217
DB 137 FWTGLDENQEGEMQWVDGDTTRSSFTFMKEGEPNNKGFNEDCAHV-----WTSGQW 188
QY 218 NDVNCLEGPORSVCE 231
DB 189 NDVYCYTECYVCE 202

RESULT 6
LECT_HUMAN STANDARD: PRT; 311 AA.
3D LECL_HUMAN 000448: 003969;
AC P07307: 000448: 003969;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Asialoglycoprotein receptor 2 (Hepatic lectin H2) (ASGP-R) (ASGPR).
GN ASGR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
PI [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=86016723; PubMed=3863106;
RA Spies M., Lodish H.F.;
RT "Sequence of a second human asialoglycoprotein receptor: conservation
RT of two receptor genes during evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 82:6465-6469(1985).
[2]
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
KC TISSUE=Liver;
RX MEDLINE=92184202; PubMed=1371982;
RA Paletta E., Stockert R.J., Racevskis J.;
RT "Differences in the abundance of variably spliced transcripts for the
RT second asialoglycoprotein receptor polypeptide, H2, in normal and
RT transformed human liver."
RL Hepatology 15:395-402(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatkover L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.D., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
CC WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX
CC CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES
CC TERMINAL GALACTOSE AND N-ACETYLGLUCOSAMINE UNITS. AFTER LIGAND
CC BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
CC TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE
CC DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
CC SURFACE.
CC -1- SUBUNIT: THE FUNCTIONING LIGAND-BINDING UNIT OF THIS RECEPTOR IS
CC THOUGHT TO BE AT LEAST A DIMER.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-3:
CC Name=1;
CC IsoId=P07307-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P07307-2; Sequence=VSP_003060;
CC Name=3;
CC IsoId=P07307-3; Sequence=VSP_003060, VSP_003061;
CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
CC CELLS.
CC -1- MISCELLANEOUS: CALCULON 1 C-TYPE LECTIN FAMILY DOMAIN.
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CC -----
CC EMBL: M11025; AAB59519.1; -
CC EMBL: U97197; AAB58308.1; -
CC EMBL: X55283; CAA38997.1; -
CC EMBL: BC017251; AAH17251.1; -
CC PIR: A25179; LNH02A.
CC HSSP: P06734; IHLI.
CC Genew: HGNC:743; ASGR2.
CC MIM: 108361; -
CC GO: GO:0004873; F:asialoglycoprotein receptor activity; TAS.
CC GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
CC InterPro: IPR001304; Lectin_C.
CC InterPro: IPR005640; Lectin_N.
CC Pfam: PF00059; Lectin_C; 1.
CC Pfam: PF03954; Lectin_N; 1.
CC SMART: SM00034; LECT: 1.
CC PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
CC PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
CC Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
CC Calcium; Signal-anchor; Phosphorylation; Alternative splicing.
CC CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 80 311 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 176 302 C-TYPE LECTIN (LONG FORM).
FT SITE 5 8 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT DISULFID 177 188 BY SIMILARITY.
FT DISULFID 205 300 BY SIMILARITY.
FT DISULFID 278 292 BY SIMILARITY.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .).
FT MOD_RES 12 12 PHOSPHORYLATION.

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FT VARSPLIC 24 42 Missing (in isoform 2 and isoform 3).
 FT VARSPLIC 82 86 /FTID-VSP_003060.
 FT VARSPLIC 82 86 Missing (in isoform 3).
 FT VARSPLIC 82 86 /FTID-VSP_003061.
 SQ SEQUENCE 311 AA; 35191 MW; 82C78FEC8FEB316 CRC64;
 Query Match 17.5%; Score 223.5; DB 1; Length 311;
 Best Local Similarity 35.6%; Pred. No. 3.6e-12;
 Matches 48; Conservative 20; Mismatches 52; Indels 15; Gaps 4;
 OY 104 SCCPKNWKSESSNCFTIESASWODEKDCARMEAHLLVINTOEEDFTFONLQESAY 163
 DB 175 TCCPVNWEHOSGCTWFSHSGKAMAEERYCOLENNHVLVINSWEOKFTVOHTNPENTW 234
 OY 164 FVGLSDPEGQRHOMVQDTPYNESSTFWHPRPSD-----PNEKCVVINFKSPKRWG 216
 DB 235 -IGLIDSDGS--WKWVDGTDYRHNYKNMAVTPQPDNMHGHGLGSGEDCEVQ-----PDGR 286
 217 WMDVNCIGRQSRVCE 231
 111 111 111
 287 WMDDFCLQYRWVCE 301
 RESULT 7
 LECH_HUMAN STANDARD; PRT: 290 AA.
 ID LECH_HUMAN P07306;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Asialoglycoprotein receptor 1 (Hepatic lectin II) (ASGPR) (ASGP-R).
 GN ASGRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85130911; PubMed=2982798;
 RA Spleen M., Schwartz A.L., Lodish H.F.;
 RT "Sequence of human asialoglycoprotein receptor cDNA. An internal
 RT signal sequence for membrane insertion.";
 RL J. Biol. Chem. 260:1979-1982(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86079574; PubMed=3753585;
 RA Spleen M., Lodish H.F.;
 RT "An internal signal sequence: the asialoglycoprotein receptor membrane
 RT anchor.";
 RL Cell 44:177-185(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Wang H., Gao X., Li L., Lou H., Huang Y., Wang B., Han J.;
 RT "Human asialoglycoprotein receptor 1 gene is expressed in SH-SY5Y
 RT human neuroblastoma cells.";
 RL Submitted (Sep-2001) to the EMBL/Genbank/DBI databases.
 CC -!- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
 CC WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX
 CC CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES
 CC TERMINAL GALACTOSE AND N-ACETYLGLUCOSAMINE UNITS. AFTER LIGAND
 CC BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
 CC TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE
 CC DISSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
 CC SURFACE.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
 CC CELLS.
 CC -!- PTM: PHOSPHORYLATED ON A CYTOPLASMIC SER RESIDUE.
 CC -!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC
 CC EMBL: M10058; AAA51785.1;
 DR EMBL: AB070933; BAB83508.1;
 DR PIR: A22509; LNH01.
 DR PDB: 1D8: 26-JUL-00.
 DR GeneW: HGNC:742; ASGRI.
 DR MIM: 108360;
 DR GO: 0005887; C: integral to plasma membrane; TAS.
 DR GO: 0004873; F: asialoglycoprotein receptor activity; TAS.
 DR GO: 0006898; P: receptor mediated endocytosis; TAS.
 DR InterPro: IPR002353; Antifreeze1.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR005640; Lectin_N.
 DR Pfam: PF00059; Lectin_C; 1.
 DR Pfam: PF03954; Lectin_N; 1.
 DR PRINTS: PR00356; ANTI-FREEZE1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00645; C-TYPE_LLECTIN_1; 1.
 DR PROSITE: PS00641; C-TYPE_LLECTIN_2; 1.
 KW Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane; Calcium;
 KW Signal-anchor; Phosphorylation; 3D-structure.
 FT INIT_MET 0
 FT DOMAIN 1 39
 FT TRANSMEM 40 60
 FT DOMAIN 61 290
 FT DOMAIN 152 278
 FT SITE 4 7
 FT DISULFID 153 164
 FT DISULFID 181 276
 FT DISULFID 254 268
 FT CARBOHYD 80 80
 FT CARBOHYD 148 148
 SQ SEQUENCE 290 AA; 33055 MW; B1897CB30DAE1586 CRC64;
 Query Match 17.2%; Score 220.5; DB 1; Length 290;
 Best Local Similarity 28.8%; Pred. No. 6e-12;
 Matches 51; Conservative 28; Mismatches 75; Indels 23; Gaps 6;
 OY 70 QKYSQLEKTKTELVHT-----TLECVKKNMFEETANSCCPKNKKSFSSNCFYS 121
 DB 109 EKQKQKLSHDSHSLILHVKQFVSDLRSLSCQMAALOGNCSERTCCPVNWEHRSQYMS 168
 OY 122 TESASWODEKDCARMEAHLLVINTOEEDFTFONLQESAYFVGLSDPEGQRHOMVQ 181
 DB 169 RSGKAWADADNYCRLEDAHLVYVTSWEQKQFVQHHIGPVNTW-MGLHDNGP--WKWVDG 225
 OY 182 TPYNESSTFWHPRPSD-----PNEKCVVINFKSPKRWGMNDVNCIGRQSRVCE 231
 DB 226 TIVETGFKWVRPQPDWYGHGLGSGEDCA--HFTDDGR---WMDVCGRPYRWVCE 277
 RESULT 8
 LECH_MOUSE STANDARD; PRT: 283 AA.
 ID LECH_MOUSE P34927; O64363;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Asialoglycoprotein receptor 1 (Hepatic lectin I) (MHL-1) (ASGP-R)
 GN ASGRI OR ASGR-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

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Db      101  NLVSKLEKQCKDLDLEHSSLLHLVHKQVSDVSRLSQGMAFRNGSRICCPINWVEYE 160
OY      115  SNCFYFISTESASWODESEKDCARMAHLIVNTQOEODFIFONLQESAYEYGLSDPEGOR 174
Db      161  GSCYWFSSSVYPMTEADKXCCOLENAHLIVVTSRDEONFLORHMLPLNTW-IGLTDNGP- 218
OY      175  HMCWVVDQTPVNESSTFWHPRRPSD-----PNERCVLNRKSPKRWGWVWVCLGPQR 227
Db      219  -WKWVVDGDEYETGFQNMRRPEQPDWVWGHGLGGEDCA--HFTDGR--WMDVCCRPRYR 272
OY      228  SVCE 231
Db      273  WVCE 276

RESULT 9
MMGL_MOUSE
ID      MMGL_MOUSE      STANDARD:      PRT:      304 AA.
AC      P49300.
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Macrophage asialoglycoprotein-binding protein 1 (M-ASGP-BP)
DE      (Macrophage galactose/N-acetylgalactosamine-specific lectin) (MMGL).
GN      MGL1 OR MGL.
OS      Mus musculus. (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C3H/HeN;
RX      MEDLINE=92268032; PubMed=1587794;
RT      Sato M., Kawakami K., Osawa T., Toyoshima S.;
RT      "Molecular cloning and expression of cDNA encoding a galactose/N-
RT      acetylgalactosamine-specific lectin on mouse tumoricidal
RT      macrophages."
RL      J. Biochem. 111:331-336(1992).
RN      [2]
RP      SEQUENCE OF 102-120 AND 137-151.
RC      STRAIN=C3H/HeN;
RX      MEDLINE=89197865; PubMed=3241002;
RT      Oda S., Sato M., Toyoshima S., Osawa T.;
RT      "Purification and characterization of a lectin-like molecule specific
RT      for galactose/N-acetyl-galactosamine from tumoricidal macrophages."
CC      J. Biochem. 104:600-605(1988).
CC      -1- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE
CC      DUNTS. MAY PARTICIPATE IN THE INTERACTION BETWEEN TUMORICIDAL
CC      MACROPHAGES AND TUMOR CELLS.
CC      -1- SUBUNIT: HOMO-OLIGOMER.
CC      -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC      -1- TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE OF ACTIVATED
CC      MACROPHAGES.
CC      -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: S36676; AAB22171.1; -.
DR      PIR: JX0209; JX0209.
DR      HSSP: P06734; 1H1I.
DR      MGD: MGI:96975; Mgl1.
DR      InterPro: IPR002353; Antifreeze211.
DR      InterPro: IPR01304; lectin_C.
DR      InterPro: IPR005640; lectin_N.
DR      Pfam: PF00059; lectin_C_1.
DR      Pfam: PF03954; lectin_N_1.
DR      PRINTS: PR00356; ANTIFREEZE211.

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DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE; PS00411; C-TYPE_LECTIN_2; 1.
 KW Lectin; Glycoprotein; Transmembrane; Lectin; signal-anchor.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 57 304 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 172 298 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 173 184 BY SIMILARITY.
 FT DISULFID 201 296 BY SIMILARITY.
 FT DISULFID 274 288 BY SIMILARITY.
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 304 AA; 34596 MW; 3F79CD12C34F5BCC CRC64;
 Query Match 16.9%; Score 216.5; DB 1; Length 304;
 Best Local Similarity 31.1%; Pred. No. 1.4e-11;
 Matches 47; Conservative 25; Mismatches 64; Indels 15; Gaps 5;
 89 LECVKNMPEETAWSCCPKMKSFSSNCYFISTESASWQSEKDCARMEAHLLVINTOE 148
 156 LFCQLANLNKNGSEVACPLHWTHEGSCYWFSESKSPEDAKYRLNSHLVYVNSLE 215
 149 EDDFETQNIQESATFVGLSDPEGORHQMWDQTPYNESSTWHPRESD-----PNE 201
 216 EGNFL-QNRLANVVSIGLTDNGP--WRWVDGTDPEKGFKNWAPLPDNNWFGHIGGGE 272
 202 RCVLNFRKSPKRWGNDVNCIGPORSVCEM 232
 273 DCAHIT-TGGP-----WDDVOCRTFRWCEM 298
 Db 273 DCAHIT-TGGP-----WDDVOCRTFRWCEM 298
 RESULT 10
 KUCR.MOUSE
 ID KUCR.MOUSE STANDARD; PRT; 548 AA.
 AC P70194;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-type lectin 13 (Kupffer cell receptor).
 GN CLEC5F13 OR KCLR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Takezawa R., Magatsuna H., Momoto C., Watanabe Y., Akaike T.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND FUCOSE.
 CC COULD BE INVOLVED IN ENDOCYTOSIS.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: KUPFFER CELLS.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
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 CC -----
 DR EMBL; D88577; BAA13647.1; -
 DR HSSP; P20693; 1HLT
 DR MGD; MGI:1859634; Clec5f13.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR00356; ANTIFREEZEII.
 DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE; PS00411; C-TYPE_LECTIN_2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Lectin; signal-anchor;
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 70 548 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 438 538 C-TYPE LECTIN (SHORT FORM).
 FT DISULFID 440 536 BY SIMILARITY.
 FT DISULFID 516 528 BY SIMILARITY.
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 548 AA; 61268 MW; 6F6495E820E73BD9 CRC64;
 Query Match 16.6%; Score 213; DB 1; Length 548;
 Best Local Similarity 30.6%; Pred. No. 5.5e-11;
 Matches 45; Conservative 25; Mismatches 61; Indels 16; Gaps 4;
 93 KKNMPEETAWSCCPKMKSFSSNCYFISTESASWQSEKDCARMEAHLLVINTOEQDF 152
 399 KOEKTQNOVLQILQNMKRYFNNGFYFSDRDKPMWEAKFCTSGCAHLASVTSOEQAF 458
 153 IFQNIQESATFVGLSDPEGORHQMWDQTPYN--ESSFWHPRESD-----PNEVCV 204
 459 LVQT-TSSDHWIGLTDQTEGIWRVVDTPPNNAOSKGFQGNKQDPNRRHNGEREDCV 517
 205 VLNFRKSPKRWGNDVNCIGPORSVCE 231
 518 HV-----RQQMDMACGSSYPWCK 537
 Db 518 HV-----RQQMDMACGSSYPWCK 537
 RESULT 11
 FCE2.MOUSE
 ID FCE2.MOUSE STANDARD; PRT; 331 AA.
 AC P20693; O61556; O61557;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Low affinity immunoglobulin epsilon Fc receptor (Lymphocyte IGE
 DE receptor) (Fc-epsilon-RI) (CD23).
 GN FCER2 OR FCER2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE-90017519; PubMed-2529542;
 RA Bettler B., Hofstetter H., Rao M., Yokoyama W.M., Kilcherr F.,
 RA Conrad D.H.;
 RT "Molecular structure and expression of the murine lymphocyte low-
 RT affinity receptor for IGE (Fc epsilon RI)".
 RT Proc. Natl. Acad. Sci. U.S.A. 86:7566-7570(1989).
 [2]
 SEQUENCE FROM N.A.
 RX MEDLINE-90171598; PubMed-2137845;
 RA Golinick S.O., Trounstein M.L., Yamashita L.C., Kehry M.R.,
 RA Moore K.W.;
 RT "Isolation, characterization, and expression of cDNA clones encoding
 RT the mouse Fc receptor for IGE (Fc epsilon RI)".
 RT J. Immunol. 144:1974-1982(1990).
 [3]
 SEQUENCE FROM N.A. (ISOFORMS B AND C).
 RC STRAIN=DNA/2;
 RX MEDLINE-94372613; PubMed-8086828;
 RA Kondo H., Ichikawa Y., Nakamura K., Tsuchiya S.;
 RT "Cloning of cDNAs for new subtypes of murine low-affinity Fc receptor
 RT for Ige (Fc epsilon RI/CD23)".


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RM Int. Arch. Allergy Immunol. 105:38-48(1994).
RL [4]
RN 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
RP MEDLINE=94191542; PubMed-8142907;
RX Padlan E.A., Heim B.A.;
RT "Modeling of the lectin-homology domains of the human and murine low-
  affinity Fc epsilon receptor (Fc epsilon RI/CD23).";
  Receptor 3:335-341(1993).
RL
CC -1- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION OF
  ICE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS A B-
  CELL-SPECIFIC ANTIGEN) .
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
  Event-Alternative splicing; Named isoforms-3;
  Name-A;
  IsoId=p20693-1; Sequence=Displayed;
  Name-B;
  IsoId=p20693-2; Sequence=VSP_003058;
  Name-C;
  IsoId=p20693-3; Sequence=VSP_003059;
CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR IGE, WHICH
  DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON
  BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES
  AND MONOCYTES.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
-----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: M99371; AAA74898.1; -
DR EMBL: M34163; AAA37603.1; -
DR EMBL: X64223; CAA45532.1; -
DR EMBL: X64224; CAA45533.1; -
DR PIR: A43518; LNMSEK.
DR PDB: 1HLJ; 3I-JAN-94.
DR MGD: MGI:95497; Fcgr2a.
DR InterPro: IPR002353; Antifreezeell.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C.1.
DR PRINTS: PRO0356; ANTIFREEZEII.
DR SMART: SMO0034; CLECT. 1.
DR PROSITE: PS000615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
DR Ige-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell;
  Repeat; Lectin; Signal-anchor; Alternative splicing; 3D-structure.
  CYTOPLASMIC (POTENTIAL).
  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  (POTENTIAL).
  EXTRACELLULAR (POTENTIAL).
  C-TYPE LECTIN (LONG FORM).
FT DOMAIN 50 331
FT DOMAIN 185 298
FT REPEAT 71 91
FT REPEAT 92 112
FT REPEAT 113 133
FT DISULFID 183 311
FT DISULFID 186 317
FT DISULFID 188 319
FT DISULFID 214 305
FT DISULFID 282 296
FT CARBOHYD 65 65
FT CARBOHYD 114 114
FT VASPLIC 1 7
FT VASPLIC 1 7
FT VASPLIC 1 7
FT STRAND 197 200
FT HELIX 207 216
FT TURN 217 218
FT STRAND 220 221

```

Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
HELIX	227	237	16.38	208.5	331	23	8
TURN	238	239	31.28	7.6e-11			
STRAND	242	247	34	60			
TURN	249	250					
TURN	252	253					
STRAND	256	257					
TURN	258	259					
STRAND	260	262					
STRAND	268	268					
TURN	270	271					
TURN	277	278					
STRAND	282	285					
TURN	287	288					
STRAND	291	294					
TURN	296	297					
STRAND	304	307					
SEQUENCE	331 AA	37647 MM	B8C6D5F34ACDB2 CRC64				
Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
HELIX	227	237	16.38	208.5	331	23	8
TURN	238	239	31.28	7.6e-11			
STRAND	242	247	34	60			
TURN	249	250					
TURN	252	253					
STRAND	256	257					
TURN	258	259					
STRAND	260	262					
STRAND	268	268					
TURN	270	271					
TURN	277	278					
STRAND	282	285					
TURN	287	288					
STRAND	291	294					
TURN	296	297					
STRAND	304	307					
SEQUENCE	331 AA	37647 MM	B8C6D5F34ACDB2 CRC64				

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CC EMBL: J03734; AAA41472.1; -

DR EMBL: M55533; AAA40892.1; -

DR PIR: A38674; A28166.

DR HSSP: P20693; 1HLJ.

DR InterPro: IPR002353; AntifreezeII.

DR InterPro: IPR001304; Lectin_C.

DR Pfam: PF00059; Lectin_C.1.

DR PRINTS: PR00356; ANTIFREEZEII.

DR SMART: SM00034; CLECT.1.

DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.

DR PROSITE: PS0041; C-TYPE_LECTIN_2; 1.

KW Receptor; Transmembrane; Glycoprotein; Lectin; Signal-anchor; Endocytosis.

FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 70 550 EXTRACELLULAR (POTENTIAL).

FT DISULFID 438 538 C-TYPE LECTIN (SHORT FORM).

FT DISULFID 516 528 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SQUENCE 550 AA; 61104 MW; 9358A6C4C306270 CRC04;

Query Match 15.38; Score 196; DB 1; Length 550;
Best Local Similarity 31.88; Pred. No. 1.6e-09;
Matches 42; Conservative 23; Mismatches 51; Indels 16; Gaps 4;

QY 108 KMKKSSNCFYFSTSSASMODEKCAKMEALHYINIOEDDFPQNIQESAFVGL 167
DB 414 QDKRYNGKRYFSRKSKSHENFCVSGALASVTSQEEAFVQ-ITNAVDMHTGL 472
QY 168 SPEGQRHQQWVDQF--YNESSTFWHPREPSD-----PNERCVLVNFKSPKRWGMD 219
DB 473 TDGGTGNRWVDGTFEDYVQSRFRKKGPDWNRGNGREDCVHLQRM-----WMD 525
QY 220 VNCIGQRVSCE 231
DB 526 MACGTAYNMWCK 537

RESULT 13
PCGN_MOUSE STANDARD: PRT; 1268 AA.

AC P55066;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neutocan core protein precursor (Chondroitin sulfate proteoglycan 3).
GN CSp3 OR NCAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=96039250; PubMed=7490074;
RA Rauch U., Grimpe B., Kulpe G., Arnold-Ammer I., Beler D., Faessler R.,
RT "Structure and chromosomal localization of the mouse neutocan gene",
RL Genomics 28:405-410(1995).
CC -i- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NC-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic acid.

CC -i- TISSUE SPECIFICITY: BRAIN.

CC -i- SIMILARITY: Contains 1 Immunoglobulin-like V-type domain.

CC -i- SIMILARITY: Contains 2 EGF-like domains.

CC -i- SIMILARITY: Contains 2 link domains.

CC -i- SIMILARITY: Contains 1 C-type lectin family domain.

CC -i- SIMILARITY: Contains 1 Sushi (SCR) domain.

CC -i- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.

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CC EMBL: X64727; CA59216.1; -

DR PIR: S52781; S52781.

DR HSSP: P00740; 1EDM.

DR MGD; MG1:104694; Csp3.

DR InterPro: IPR002353; AntifreezeII.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000742; EGF-2.

DR InterPro: IPR001861; EGF_Ca.

DR InterPro: IPR006209; EGF_Like.

DR InterPro: IPR007110; Ig_Like.

DR InterPro: IPR003599; Ig.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR001304; Lectin_C.

DR InterPro: IPR000338; Link.

DR InterPro: IPR000436; Sushi_SCR_CCP.

DR Pfam: PF00008; EGF; 2.

DR Pfam: PF00047; Ig; 1.

DR Pfam: PF00059; Lectin_C; 1.

DR Pfam: PF00084; sushi; 1.

DR PRINTS: PR01265; LINKMODULE.

DR PRINTS: PR00356; ANTIFREEZEII.

DR PRODOM: PD000918; Link; 2.

DR SMART: SM00034; CCEPT.1.

DR SMART: SM00179; EGF_CA; 1.

DR SMART: SM00409; IG; 1.

DR SMART: SM00445; LINK; 2.

DR PROSITE: PS00010; ASX_HYDROXYL; 1.

DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.

DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.

DR PROSITE: PS00022; EGF_1; 3.

DR PROSITE: PS01186; EGF_2; 1.

DR PROSITE: PS01187; EGF_CA; 1.

DR PROSITE: PS50835; IG_Like; 1.

DR PROSITE: PS01241; LINK; 2.

KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 1268 NEUTROCAN CORE PROTEIN.

FT DOMAIN 37 157 IG-LIKE V-TYPE.

FT DOMAIN 158 253 LINK 1.

FT DOMAIN 259 355 LINK 2.

FT DOMAIN 960 996 EGF-LIKE 1.

FT DOMAIN 998 1034 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 1036 1165 C-TYPE LECTIN.

FT DOMAIN 1166 1224 SUSHI.

FT DISULFID 58 139 BY SIMILARITY.

FT DISULFID 181 252 BY SIMILARITY.

FT DISULFID 205 226 BY SIMILARITY.

FT DISULFID 279 324 BY SIMILARITY.

FT DISULFID 303 324 BY SIMILARITY.

FT DISULFID 964 975 BY SIMILARITY.

FT DISULFID 969 984 BY SIMILARITY.

FT DISULFID 986 995 BY SIMILARITY.

FT DISULFID 1040 1051 BY SIMILARITY.

FT DISULFID 1068 1160 BY SIMILARITY.

FT DISULFID 1136 1152 BY SIMILARITY.
 FT DISULFID 1167 1210 BY SIMILARITY.
 FT DISULFID 1196 1223 BY SIMILARITY.
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 742 742 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 978 978 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1175 1175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 1268 AA; 137200 MW; 3014EBE202A2FAEC CRC64;
 Query Match 14.68; Score 187; DB 1; Length 1268;
 Best Local Similarity 32.58; Pred. No. 2.5e-08;
 Matches 39; Conservative 21; Mismatches 50; Indels 10; Gaps 4;
 QY 106 CPKMKFSNCKCFITESASQWDEKCAEMAHLLVIMQEDFIFQNLQESAYFV 165
 Db 1040 CDGGMHFGCHCYRFPNRAEMAEKDCRRAGHLTSVSPHAKTNSFGHENS--WI 1097
 QY 166 GLSDPEGQRHMOWDQTPYNESSTFMHREPSD---PNEKQVLLNFKSPKRMGMDVNC 222
 Db 1098 GLNDRYVERDFQWTDNTGLQYEN--WREKQPDNPFAGGEDCVVVAHESGR---WMDVPC 1152
 RESULT 14
 ID PCGN_RAT STANDARD; PRT; 1257 AA.
 AC P55067;
 DT 01-OCT-1996 (Rel. 34, Last Created)
 DT 01-OCT-1996 (Rel. 42, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
 DS (245 kDa early postnatal core glycoprotein) [contains: 150 kDa adult
 DE core glycoprotein].
 GN CSRG3 OR NCAN.
 OS Rattus norvegicus (Rat).
 OC Eumetazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;
 RX MEDLINE=92406907; PubMed=1326537;
 RA Rauch U., Karthikeyan L., Maurel P., Margolis R.O., Margolis R.K.;
 RT Cloning and primary structure of neurocan, a developmentally
 RT regulated, aggregating chondroitin sulfate proteoglycan of brain.;
 RL J. Biol. Chem. 267:19536-19547(1992).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=94230574; PubMed=7513709;
 RT Friedlander D.R., Miley P., Karthikeyan L., Margolis R.K.,
 RT Margolis R.U., Grunet M.;
 RT "The neuronal chondroitin sulfate proteoglycan neurocan binds to the
 RT neural cell adhesion and neurite outgrowth.";
 RL J. Cell Biol. 125:669-680(1994).
 CC - FUNCTION: May modulate neuronal adhesion and neurite growth during
 CC development by binding to neural cell adhesion molecules (NG-CAM
 CC and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
 CC acid.
 CC - TISSUE SPECIFICITY: EARLY POSTNATAL AND ADULT BRAIN; NOT EXPRESSED
 CC IN KIDNEY, LUNG, LIVER AND MUSCLE.
 CC - PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND
 CC O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
 CC - PTM: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC
 CC DEGRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL
 CC BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.
 CC - SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC - SIMILARITY: Contains 2 EGF-like domains.
 CC - SIMILARITY: Contains 1 C-type lectin family domain.
 CC - SIMILARITY: Contains 1 sushi (SCR) domain.
 CC - SIMILARITY: BELONGS TO THE AGGREGAN/VERSICAN PROTEOGLYCAN FAMILY.
 CC

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 CC -----
 DR EMBL: M97161; AAC37679.1; -.
 DR PIR: S28764; S28764.
 DR HSSP: P00740; IDEM.
 DR InterPro: IPR002353; Antifreeze2.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR000538; Link.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00059; Lectin_C_1.
 DR Pfam: PF00084; sushi_1.
 DR Pfam: PF00193; XLink_2.
 DR PRINTS: PR01265; LINKMODULE.
 DR PRINTS: PR00356; ANTIFREEZE2.
 DR PRODOM: PD000918; Link_2.
 DR SMART: SM00032; CCP_1.
 DR SMART: SM00034; CLECT_1.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00409; Ig_1.
 DR SMART: SM00445; Link_2.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
 DR PROSITE: PS00022; EGF_1; 3.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS50835; IG-LIKE_1.
 DR PROSITE: PS01241; LINK_2.
 KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
 KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 1257
 FT CHAIN 639 1257
 FT DOMAIN 37 157
 FT DOMAIN 158 253
 FT DOMAIN 259 355
 FT DOMAIN 949 985
 FT DOMAIN 987 1023
 FT DOMAIN 1025 1154
 FT DOMAIN 1155 1213
 FT DISULFID 58 139
 FT DISULFID 181 252
 FT DISULFID 205 226
 FT DISULFID 279 354
 FT DISULFID 303 324
 FT DISULFID 953 964
 FT DISULFID 973 973
 FT DISULFID 975 984
 FT DISULFID 1029 1040
 FT DISULFID 1057 1149
 FT DISULFID 1125 1141
 FT DISULFID 1185 1199
 FT DISULFID 1186 1212
 FT CARBOHYD 121 121
 FT CARBOHYD 121 121
 FT CARBOHYD 339 339
 FT CARBOHYD 737 737
 FT CARBOHYD 944 944
 FT CARBOHYD 967 967
 NEUROCAN CORE PROTEIN.
 150 kDa ADULT CORE GLYCOPROTEIN.
 IG-LIKE V-TYPE.
 LINK 1.
 LINK 2.
 EGF-LIKE 1.
 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 C-TYPE LECTIN.
 SUSHI.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 O-LINKED (XYL. . .) (CHONDROITIN SULFATE).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1164 1164 N-LINKED (GLCNAC..) (POTENTIAL).
 SQ SEQUENCE 1257 AA; 135544 MW; 992B33DCFA19EE1B CRC64;
 Query Match 14.4%; Score 184; DB 1; Length 1257;
 Best Local Similarity 31.7%; Pred. No. 4.5e-08;
 Matches 38; Conservative 22; Mismatches 50; Indels 10; Gaps 4;
 QY 106 CPKMKSFSSNCYFISTESASWDSKDCARMEAHLLVINTOEODFIFONLQESAYEV 165
 DB 1029 CDGWMKFGCHCYRYFAHRAWEDAEKDCRRRAGHLTSVSPDEHFFINSFGHENS--WI 1086
 QY 166 GLSDPEGRHMQWVDOTPYNESSTFWHPRPSD---PNEKCVLNRKSPKRGWMDVNC 222
 DB 1087 GLNDRIVERDFQWTDNTGLQYEN--WREKQPDNFAGGEDCVYVAHENGMR---WMDVPC 1141
 RESULT 15
 PGCN_HUMAN STANDARD; PRT; 1321 AA.
 014594; Q90PK6;
 28-FEB-2003 (Rel. 41, Created)
 28-FEB-2003 (Rel. 41, Last sequence update)
 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
 GN CSFG3 OR NCAN OR NEUR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99013874; PubMed=9795216;
 RA Prange C.K., Pennacchio L.A., Ikenai K., Fan W., Lennon G.G.;
 RT "Characterization of the human neurocan gene, CSFG3.";
 RL Gene 221:199-205(1998).
 [2]
 RP SEQUENCE OF 1-990 AND 1007-1321 FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
 RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,
 RA Danghan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
 RA Liu S., Atlix C., Andreise T., Frankheim M., Amico-Keller G.,
 RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
 RA Kobayashi A., Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of an ~1 Mb region containing the MEF2B gene in
 19p12.";
 RA Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May modulate neuronal adhesion and neurite growth during
 development by binding to neural cell adhesion molecules (NG-CAM
 and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronate
 acid.
 CC -1- TISSUE SPECIFICITY: Brain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -1- SIMILARITY: Contains 2 link domains.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -1- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -1- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL; AF026547; AAC80576.1; -
 DR EMBL; AC003110; AAB86655.1; -
 DR EMBL; AC005254; AAC25581.1; -
 DR HSSP; P00740; 1EDM.
 DR Genew; HGNC:2465; CSFG3.

DR MIM; 600826; -
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR00538; Link.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00059; lectin_C_1.
 DR Pfam: PF00084; sushi_1.
 DR Pfam: PF00193; Xlink_2.
 DR PRINTS: PR01265; LINKMODULE.
 DR PRODOM: PD000918; Link_2.
 DR SMART: SM00032; CCP_1.
 DR SMART: SM00034; CLECT_1.
 DR SMART: SM00179; EGF_CA_1.
 DR SMART: SM00409; IG_1.
 DR SMART: SM00445; LINK_2.
 DR PROSITE: PS00010; ASX_HYDROXYL_1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1.
 DR PROSITE: PS00041; C_TYPE_LLECTIN_2; 1.
 DR PROSITE: PS00022; EGF_1; 3.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA_1.
 DR PROSITE: PS00835; IGLIKE_1.
 DR PROSITE: PS01241; LINK_2.
 KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
 EGF-like domain; Calcium; Repeat; Sushi; signal.
 FT SIGNAL 1 22
 FT CHAIN 23 1321
 FT DOMAIN 38 153
 FT DOMAIN 159 254
 FT DOMAIN 260 356
 FT DOMAIN 1008 1044
 FT DOMAIN 1046 1082
 FT DOMAIN 1084 1213
 FT DOMAIN 1214 1272
 FT DISULFID 59 140
 FT DISULFID 182 253
 FT DISULFID 206 227
 FT DISULFID 280 355
 FT DISULFID 304 325
 FT DISULFID 1012 1023
 FT DISULFID 1017 1032
 FT DISULFID 1034 1043
 FT DISULFID 1088 1099
 FT DISULFID 1116 1208
 FT DISULFID 1184 1200
 FT DISULFID 1215 1258
 FT DISULFID 1244 1271
 FT CARBOHYD 122 122
 FT CARBOHYD 340 340
 FT CARBOHYD 1026 1026
 FT CARBOHYD 1223 1223
 FT CARBOHYD 1234 1234
 FT CONFLICT 1254 1254
 FT CONFLICT 1282 1282
 SQ SEQUENCE 1321 AA; 142972 MW; 2EF47F823DB980B8 CRC64;
 Query Match 14.4%; Score 184; DB 1; Length 1321;
 Best Local Similarity 32.5%; Pred. No. 4.8e-08;
 Matches 39; Conservative 20; Mismatches 51; Indels 10; Gaps 4;
 QY 106 CPKMKSFSSNCYFISTESASWDSKDCARMEAHLLVINTOEODFIFONLQESAYEV 165
 DB 1088 CDGWMKFGCHCYRYFAHRAWEDAEKDCRRRAGHLTSVSPDEHFFINSFGHENT--WI 1145
 QY 166 GLSDPEGRHMQWVDOTPYNESSTFWHPRPSD---PNEKCVLNRKSPKRGWMDVNC 222

Db 1146 GLNDRIVERDFOWTDNGLQFEN--WRENQPDNFFAGGEDCVVVAHESGR---WMDVPC 1200

Search completed: August 4, 2003, 13:09:09
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 13:05:28 : Search time 96 Seconds
(without alignments)
637.067 Million cell updates/sec

Title: US-09-862-802-2
Perfect score: 1280
Sequence: 1 MTSEITVAEVRFKNEFKSSG.....NDVNCGLGPRQVCEMMKIH 237

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	4 Q9UI34	Q9UI34 homo sapien
2	1275	99.6	237	4 Q9NS33	Q9NS33 homo sapien
3	1273	99.5	237	4 Q9UM7	Q9UM7 homo sapien
4	1231	96.2	230	4 Q8WXM9	Q8WXM9 homo sapien
5	1079.5	84.3	204	4 Q9H229	Q9H229 homo sapien
6	672.5	52.5	238	11 Q9GZ15	Q9GZ15 mus musculu
7	650.5	50.8	262	11 Q923C7	Q923C7 mus musculu
8	551.5	43.1	213	4 Q8WTT0	Q8WTT0 homo sapien
9	533.5	41.7	182	4 Q8WXM8	Q8WXM8 homo sapien
10	489	38.2	209	11 Q9JKE4	Q9JKE4 mus musculu
11	476.5	37.2	158	11 Q8JZX6	Q8JZX6 mus musculu
12	452.5	35.4	175	11 Q9JKE3	Q9JKE3 mus musculu
13	447	34.9	176	11 Q9D8Q7	Q9D8Q7 mus musculu
14	440.5	34.4	152	11 Q8CIG3	Q8CIG3 mus musculu
15	400	31.2	215	4 Q8NS55	Q8NS55 homo sapien
16	399	31.2	215	4 Q8WXM8	Q8WXM8 homo sapien

17	352.5	27.5	219	11 Q922H6	Q922H6 mus musculu
18	352.5	27.5	219	11 Q8C212	Q8C212 mus musculu
19	330.5	25.8	168	11 Q9JKE2	Q9JKE2 mus musculu
20	330	25.8	219	4 Q9ULX5	Q9ULX5 homo sapien
21	325.5	25.4	214	11 Q9R0Q8	Q9R0Q8 mus musculu
22	256.5	20.0	292	4 Q14538	Q14538 homo sapien
23	253.5	19.8	236	13 Q8U0M9	Q8U0M9 oryzae lat
24	253	19.8	316	4 Q8IUN9	Q8IUN9 homo sapien
25	243	19.0	208	11 Q912W7	Q912W7 mus musculu
26	233	18.2	237	11 Q912W8	Q912W8 mus musculu
27	232	18.1	263	4 Q96QP3	Q96QP3 homo sapien
28	232	18.1	376	4 Q9BX53	Q9BX53 homo sapien
29	232	18.1	399	4 Q9H2X3	Q9H2X3 homo sapien
30	230.5	18.0	332	4 Q96QP5	Q96QP5 homo sapien
31	230	18.0	256	6 Q8MIS5	Q8MIS5 macaca mula
32	230	18.0	399	6 Q8HY12	Q8HY12 hylobates l
33	230	18.0	399	6 Q8HY10	Q8HY10 hylobates c
34	226	17.7	422	6 Q8HY11	Q8HY11 hylobates s
35	225	17.6	381	6 Q8HY02	Q8HY02 hylobates s
36	224	17.5	445	6 Q8HY05	Q8HY05 pan troglod
37	223	17.4	238	11 Q912X1	Q912X1 mus musculu
38	223	17.4	376	6 Q8HY06	Q8HY06 gorilla gor
39	223	17.4	445	6 Q8HYC0	Q8HYC0 pan troglod
40	221	17.3	284	11 Q91Y84	Q91Y84 mus musculu
41	221	17.3	399	4 Q9H2Q9	Q9H2Q9 homo sapien
42	219.5	17.1	322	11 Q8CJ89	Q8CJ89 mus musculu
43	219.5	17.1	742	4 Q9BYH7	Q9BYH7 homo sapien
44	217.5	17.0	417	4 Q8TCR2	Q8TCR2 homo sapien
45	217.5	17.0	742	4 Q8WZ44	Q8WZ44 homo sapien

ALIGNMENTS

RESULT 1	
Q9UI34	
AC Q9UI34:	PRELIMINARY; PRT; 237 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE C-type lectin superfamily 6.	
GN CLCSCF6.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Richard M., Beaulieu A.D.;	
RT "A novel C-type lectin expressed in GM-CSF stimulated neutrophils.";	
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AF109146; AAF14348.1; -	
DR InterPro; IPR001304; Lectin_C.	
DR Pfam; PF00059; Lectin_C; 1.	
DR SMART; SM00034; CLECT; 1.	
DR PROSITE; PS00615; C-TYPE_LLECTIN_1; 1.	
DR PROSITE; PS50041; C-TYPE_LLECTIN_2; 1.	
KW Lectin.	
SO SEQUENCE	237 AA; 27488 MW; 1A68BCE8323345BA CRC64;
Query Match	100.0%; Score 1280; DB 4; Length 237;
Best Local Similarity	100.0%; Pred. No. 8.2e-117;
Matches	237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MTSEITVAEVRFKNEFKSSGINTASSASKERTAPLKSNTPKLLCASLLIFLLLAIS 60
DB	1 MTSEITVAEVRFKNEFKSSGINTASSASKERTAPLKSNTPKLLCASLLIFLLLAIS 60
QY	61 FFIAFVIFPQKYSQLEKTKTKELVHTTLECYKKNMPVEETAWSCCPKNNKMSFSSNCYFI 120
DB	61 FFIAFVIFPQKYSQLEKTKTKELVHTTLECYKKNMPVEETAWSCCPKNNKMSFSSNCYFI 120

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QY 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNTQESATFVGLSDPEGGRHMQWVD 180
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNTQESATFVGLSDPEGGRHMQWVD 180
QY 181 QTPYNESSTFWHREPSPDNERCVLNFRRKSPKRMGNNDVCLGPORSVCEMMKIH 237
DB 181 QTPYNESSTFWHREPSPDNERCVLNFRRKSPKRMGNNDVCLGPORSVCEMMKIH 237

RESULT 2
Q9NS33 PRELIMINARY; PRT; 237 AA.
ID 09NS33
AC 09NS33
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE H0CGC13P.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA Zhao Z., Huang X., Li N., Zhu X., Cao X.;
RT "Novel gene identified from dendritic cells."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067800; AAF75560.1; -
DR Genew; HGNC:13257; CLECSE6.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
SQ SEQUENCE 237 AA; 27504 MW; 71197BFD337651EB CRC64;

Query Match 99.6%; Score 1275; DB 4; Length 237;
Best Local Similarity 99.6%; Pred. No. 2.5e-116;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MISEITVAEYRFRNFKNEKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
DB 1 MISEITVAEYRFRNFKNEKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
QY 61 FFLAFVIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCFYI 120
DB 61 FFLAFVIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCFYI 120
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNTQESATFVGLSDPEGGRHMQWVD 180
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNTQESATFVGLSDPEGGRHMQWVD 180
QY 181 QTPYNESSTFWHREPSPDNERCVLNFRRKSPKRMGNNDVCLGPORSVCEMMKIH 237
DB 181 QTPYNESSTFWHREPSPDNERCVLNFRRKSPKRMGNNDVCLGPORSVCEMMKIH 237

RESULT 3
Q9UMR7 PRELIMINARY; PRT; 237 AA.
ID 09UMR7
AC 09UMR7
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Dendritic cell immunoreceptor.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA MEDLINE=93370001; Pubmed=10438934;
RX Bates E.E., Fournier N., Garcia E., Valadeau J., Durand I., Pin J.J.,

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RA Zurawski S.M., Patel S., Abrams J.S., Lebecque S., Garrone P.,
RA Saeland S.;
RT "APCs express DCIR, a novel c-type lectin surface receptor containing
RT an immunoreceptor tyrosine-based inhibitory motif."
RL J. Immunol. 163:1973-1983(1999).
DR EMBL; AJ133532; CAB54001.1; -
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 237 AA; 27512 MW; 1D07003E4C9C9F6E CRC64;

Query Match 99.5%; Score 1273; DB 4; Length 237;
Best Local Similarity 99.6%; Pred. No. 3.9e-116;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MISEITVAEYRFRNFKNEKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
DB 1 MISEITVAEYRFRNFKNEKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
QY 61 FFLAFVIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCFYI 120
DB 61 FFLAFVIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCFYI 120
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNTQESATFVGLSDPEGGRHMQWVD 180
DB 121 STESASWQDSEKDCARMEAHLLVINTQEDDFITQNTQESATFVGLSDPEGGRHMQWVD 180
QY 181 QTPYNESSTFWHREPSPDNERCVLNFRRKSPKRMGNNDVCLGPORSVCEMMKIH 237
DB 181 QTPYNESSTFWHREPSPDNERCVLNFRRKSPKRMGNNDVCLGPORSVCEMMKIH 237

RESULT 4
Q8KXW9 PRELIMINARY; PRT; 230 AA.
ID 08KXW9
AC 08KXW9
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Fc-epsilon receptor III.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA Zhang W., Zhang J., Li N., Wan T., Chen T., Cao X.;
RT "Novel human Fc-epsilon receptor III."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF328684; AAL56016.1; -
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 230 AA; 26603 MW; 03CAB887D71BB084 CRC64;

Query Match 96.2%; Score 1231; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.8e-112;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISEITVAEYRFRNFKNEKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
DB 1 MISEITVAEYRFRNFKNEKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFFLLAIS 60
QY 61 FFLAFVIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCFYI 120
DB 61 FFLAFVIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETAMSCCPKMKSSSNCFYI 120

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QY 121 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 180
DB 121 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 180
QY 181 QTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 228
DB 181 QTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 228

RESULT 5

Q9H229 PRELIMINARY: PRT: 204 AA.
AC Q9H229: 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DN C-type lectin DB27 short form.
GN DB27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP Richard M., Beaulieu A.D.:
RT "A short ORF for the C-type lectin DB27."
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF200738; AAG3593.1; -
DR InterPro: IPR002353; Antifreeze1.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C.1.
DR PRINTS: PR000356; ANTI-FREEZE1.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 204 AA; 23550 MW; 4DFEC27549CEAAS CRC64;

Query Match 84.3%; Score 1079.5; DB 4; Length 204;
Best Local Similarity 85.7%; Pred. No. 2.5e-97;
Matches 203; Conservative 1; Mismatches 0; Indels 33; Gaps 1;

QY 1 MTSETTYAEVRPKNEFKSSGINTASSASKERTAPLKNTGPKLLCASILIFLLAIS 60
DB 1 MTSETTYAEVRPKNEFKSSGINTASSASKERTAPLKNTGPKLLCASILIFLLAIS 60
QY 61 FFIAFVIFFOKYSQLEKRTTKELVHTTLECYKKNMPYETAMSCCPKMKSSFNCFYI 120
DB 61 FFIAFVIFFOKYSQLEKRTTKELVHTTLECYKKNMPYETAMSCCPKMKSSFNCFYI 120
QY 121 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 180
DB 121 STESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORHOMWD 180
QY 181 QTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 228
DB 181 QTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 228

RESULT 6

Q9Q215 PRELIMINARY: PRT: 238 AA.
AC Q9Q215: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DN Dendritic cell immunoreceptor (C-type).
GN CLEC5F OR DCIR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymph node.
RX MEDLINE-99370001; PubMed-10436934;
RA Bates E.E., Fournier N., Garcia E., Valladeau J., Durand I., Piu J.J.,
RA Zurawski S.M., Patel S., Abrams J.S., Lebecque S., Garrone P.,
RA Saeland S.;
RT "Apc8 express DCIR, a novel C-type lectin surface receptor containing
an immunoreceptor tyrosine-based inhibitory motif."
RL J. Immunol. 163:1973-1983(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RX MEDLINE-21830942; PubMed-11841542;
RA Kanazawa N., Okazaki T., Nishimura H., Tashiro K., Inaba K.,
RA Miyachi Y.;
RT "DCIR acts as an inhibitory receptor depending on its immunoreceptor
tyrosine-based inhibitory motif."
RL J. Invest. Dermatol. 118:261-266(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-Cerebellum;
RX MEDLINE-22354683; PubMed-12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:565-573(2002).
DR EMBL: AJ133533; CAB57870.1; -
DR EMBL: AF387099; AAM22402.1; -
DR EMBL: AK049002; BAC33509.1; -
DR HSSP: P05140; ZAFP.
DR MGD: MGI:1349412; Clec5f6.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C.1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 238 AA; 27323 MW; 2DB8AE0E11B18A56 CRC64;

Query Match 52.5%; Score 672.5; DB 11; Length 238;
Best Local Similarity 53.3%; Pred. No. 1.5e-57;
Matches 129; Conservative 37; Mismatches 67; Indels 9; Gaps 6;

QY 1 MTSETTYAEVRPKNEFKSSGINTASSASKERTAPLKNTGPKLLCASILIFLLAIS 58
DB 1 MTSETTYAEVRPKNEFKSSGINTASSASKERTAPLKNTGPKLLCASILIFLLAIS 58
QY 59 ISFFIAFVIFFOKYSQLEKRTTKELVHTTLECYKKNMPYETAMSCCPKMKSSFNCFYI 117
DB 59 ISFFIAFVIFFOKYSQLEKRTTKELVHTTLECYKKNMPYETAMSCCPKMKSSFNCFYI 117
QY 118 YFIST-ESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORH 175
DB 118 YFIST-ESASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORH 175
QY 119 YLVTYSSASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORH 177
DB 119 YLVTYSSASWODSEKDCARMEAHLLVINTOEODPIFONLOESAYFVGLSDPEGORH 177
QY 176 WQWVDQTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 235
DB 176 WQWVDQTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 235
QY 178 WQWVDQTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 236
DB 178 WQWVDQTPYNESSTFWHPRPSDPNERCVLNFRRKSPKRGWMDVNCIGPQRS 236

QY 236 HL 237
DB 237 NL 238

RESULT 7

Q923C7 PRELIMINARY: PRT: 262 AA.
AC Q923C7: 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DN Similar to C-type (Calcium dependent, carbohydrate recognition domain)

Db		17	YSKYFRLSKLREYQVHYPSLICVMGEKDIED--WSCOPTPTSPSSOCVFISTGWSMT	74
Qy		129	DSEKDCAMEAHLIVINQOEODFFLONQEESATFVLGISDEGORHOMWVDOTPYNESS	188
Db		75	KSOIKSVMGADLVIVINTREEODFTIOLNKRNSSYFLGISDGGRRHMOWVDOTPENYV	134
Qy		189	TFWHPREDSDNERCVLINFPRSPRKMGINDVNCIGPORSVCENMKIHL	237
Db		135	TFWHSGEPNLDERCALLINFNS-BEWGMNDIHCHVPKSIICKMRKIYL	182
 RESULT 10				
ID	Q9JKF4		PRELIMINARY:	PRT: 209 AA.
AC	Q9JKF4;			
DR	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DEF	lectin-2 alpha isoform (C-type (Calcium dependent), carbohydrate recognition domain) lectin, superfamily member 10).			
GN	CLECSEF10.			
MS	Mus musculus (Mouse).			
SS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
SL	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCB1_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/c;			
RA	Arlizumi K., Shen G., Shikano S., Ritter R. III, Zukas P.,			
RT	"Cloning of a second dendritic cell-associated C-type lectin (lectin-			
RT	2) and its alternatively spliced isoforms."			
RL	J. Biol. Chem. 0:0(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Straubeberg R.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF240357; AAF67177.1; -			
DR	EMBL; BC023008; AAH23008.1; -			
DR	HSSP; P22897; IEGG.			
DR	MGI; MGI:1861231; Clecsef10.			
DR	InterPro; IPRO01304; Lectin_C.			
DR	Pfam; PF00059; Lectin_c_1.			
DR	SMART; SM00034; CLECT_1.			
DR	PROSITE; PS00615; C_TYPE_LECTIN_1; 1.			
DR	PROSITE; PS00441; C_TYPE_LECTIN_2; 1.			
KW	Lectin.			
SO	SEQUENCE	209 AA; 24324 MW; 7AB8BDC0DB1EA5ED CRC64;		
 Query Match				
	Best Local Similarity	38.2%; Score 489; DB 11; Length 209;		
	Matches	89; Conservative 35; Mismatches 63; Indels 10; Gaps 3		
Qy		46	LCASLLIFFLLAISFIAPVYFF-----QRKSLEKKTTTELVTHTIECYKKNMPVE	100
Db		18	IWSAAVVISLILSTCFIASCVTYOPIIDOPSRRIEYLT---YHSSLTCSSEGTWSE	73
Qy		101	TAMSCCPKMKRSFESSNCYFISTESAWDSSEKDCARMEAHLYVINTEODPIFNLOEE	160
Db		74	KMGGCCPHNMKSFGSCYLITKEKFMFSTSEQNCYGMAHLYVINTAEQNITTOQLNES	133
Qy		161	SAYFGLSDPGORHOMWVDOTPYNESSTFWHPRESDNERCVLINFKSPKRGWMDY	220
Db		134	LSYFLGLSDPGONGKMQWIDDPFEQNVRFWMHPHEPNLPBEKCVSIYV-WNNSKGWMDY	192
Qy		221	NCLGFORSVCENMKIHL	237
Db		193	FCDSKHNSICEKMKIYL	209
 RESULT 11				
ID	Q8JZX6		PRELIMINARY:	PRT: 158 AA.

Query	Subject	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	82 KEIVYTTLECYKKNPVEETAWSCCPKMKWKSFSNCFISTE-SASMODEKDCARMEAH	37.2%	DB 11	158	Best Local Similarity 53.5%, Pred. No. 1.2e-38;				
DB	4 KEINTELECYKKNASLIDKWKSCCPKMKPGSCYCTSTIDVLSWMSKNCCHMGH	30	30	40	3	3	3	3	3
QY	141 LVIVTQEOEDEFICNLQEEASVYFGLSDPEQRMQWVDQTPYNESSTFWHPREPSDN								
DB	64 LVIVHSQEOEDEFITGLDTPYAFYGLSNP-GDOOMOWIDQPPYDNDNTTFWKGPSSDN								
QY	201 ERCVVLNFRKSPKRGKNDVNCIGRGRSVCEMKIHL								
DB	123 EQCVLIINRQS-TGGMWSMDIPCSDKXNSICHVKIYL								

RESULT 12

ID	Q9JRF3	PRELIMINARY	PRT	175 AA
AC	Q9JRF3			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Declin-2 beta isoform.			
DE	CLECSF10.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
GN	NCBI_Taxid=3110037K17Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			</

Query Match	35.4%	Score 452.5	DB 11	Length 175
Best Local Similarity	43.4%	Pred. No. 3.1e-36		
Matches	82	Conservative	28	Mismatches 46; Indels 33; Gaps 3
Qy	49	SLIIFPELLATISPFIAFYIFQKYSQLEKKTTRKELVHTLTLCYKKNMPVETAMSCCPK	108	
Db	20	SAAVISMLLSTCFIA-----SCVKK-----MGCCPN	47	
Qy	109	NKSFSSNCYFISTESASMODSEKDCAMEAHLYINTQEDOFFIQLQIESAFVGLS	168	
Db	48	HMKSGSGSCYLSTSTENFNTSWSEQCYGMGAHLVYINTEADENFTIQLQNESLSTFGLS	107	
Qy	169	DPEGGRKQWYDQIPYFNESSTFFWPREPSDPERNCVILNFKRSPKRGWINDVNCIGPORS	228	
Db	108	DPOGNGKQWQIDDPFSQNVRFHHEPNLPEERCVSIVY-WNPSKGMGNDVFCDSKHS	166	
Dd	229	VCEMKKHTL 237		
	167	ICEMKKITL 175		
RESULT 13				
Q9DB07				
ID	Q9DB07	PRELIMINARY:	PRT:	176 AA.
AC	Q9DB07			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	1810046124Rik	protein.		
GN	1810046124Rik.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
QX	NCBI_Taxid=10090;			
QX	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=C57BL/6J; TISSUE=Pancreas;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,			
RA	Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikrado I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Futuro M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein S.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustiguet S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang R.H., Weitz C., Whitaker C., Wilming L.,			
RA	Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:665-690(2001).			
RL	EMBL; AK007794; BAB35260.1; -			
DR	HSSP; P05140; 2APF.			
DR	MCD; MGI:1917060; 1810046124Rik.			
DR	InterPro; IPR01304; Lectin_C.			
DR	Pfam; PF00059; Lectin_c.1.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C_Type_Lectin_1; 1.			
DR	PROSITE; PS00041; C_Type_Lectin_2; 1.			
SO	SEQUENCE 176 AA; 20342 MW; C020F749633D27BA CRC64;			
Query Match	34.9%	Score 447	DB 11	Length 176
Best Local Similarity	46.6%	Pred. No. 1.1e-35		

Matches	89: Conservative	24: Mismatches	42: Indels	36: Gaps	5
OY	49 SLIFPELLAISFIAFYVIFFOKYSQLEKTKTKELVHTTLECYVKKNNPVETANSCCPK	108			
Db	20 SAAVISTILLSTCFIA-----SCYDK-----VWSCPK	47			
OY	109 NKKSPSSNCCYIST--ESASMODSEKDCARMEAHLLVINTOEODFIFONLOESAFYVG	166			
Db	48 DMKLEFGSHCIYLPVYFSSASNNKSENCRMAHLVTHSOEDDFITGILDTHAAYTIG	107			
OY	167 LSDEGGRHMQWVDOTPYNESSTFWHPREPSDPNRCVYLNFRKSPKRGANDVNCLOPQ	226			
Db	108 LMD-TGHRQMGWVDOTPYEASVTFWHPNEPSSDNCKCYVYYRRN-IGMGWINDISCNKQ	165			
OY	227 RSVCEMAKIH L 237				
Db	166 KSVCCMKKIN L 176				
RESULT 14					
O8CIG3	PRELIMINARY;	PRT;	152 AA.		
ID	O8CIG3				
AC	O8CIG3;				
DT	01-MAR-2003 (TREMBLrel. 23, Created)				
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	C-type (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Epididymis;				
RX	MEDLINE=22354683; PubMed=12466851;				
RA	THE FANTOM Consortium,				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of				
RT	60,770 full-length cDNAs."				
RL	Nature 420:563-573(2002).				
DR	EMBL, AK020363; BAC25626.1; -.				
FT	NON-TER				
SO	SEQUENCE	152 AA; 17489 MW; 5A9646BC29FD834B CRC64;			
Query Match					
	Best Local Similarity	34.4%; Score 440.5; DB 11; Length 152;			
	Matches	81; Conservative 25; Mismatches 41; Indels 7; Gaps 4;			
OY	89 LECKKKNPV---ETANSCCPKNNKSSNNCYIST--ESASMODSEKDCARMEAHLLV	143			
Db	1 LESIEITDGIILAPEKQVWSCPKPMRLGSHCIYLPVYSSASNNKSENCRMAHLV	60			
OY	144 INPDEODFIFONLOESAFYVGLSDPGGRHMQWVDOTPYNESSTFWHPREPSDPNRC	203			
Db	61 IQSOEDDFITGILDTHAAYTIGLMD-TGHRQMGWVDOTPYEESTITFMHNEPSSGNKRC	119			
OY	204 VLVNFRKSPKRGANDVNCLOPQRSVCEMAKIH L 237				
Db	120 ATIIYRMK-TGMRWINDISCLKRSVCCMKKIN L 152				
RESULT 15					
O8NSJ5	PRELIMINARY;	PRT;	215 AA.		
ID	O8NSJ5				
AC	O8NSJ5;				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	C-type lectin-like receptor.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				

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OM protein - protein search, using sw model

Run on: August 4, 2003, 12:55:42 ; Search time 85 Seconds

(without alignments)
442.567 Million cell updates/sec

Title: US-09-862-802-2

Perfect score: 1280

Sequence: 1 MTSEITYAEVFRKNEKSSG.....NDVNCIGPQSRVCEMMKTHL 237

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_19Jun03.*
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	20 AAW88124	Primate DCMPI C-1e
2	1275	99.6	237	23 ABB90277	Human polypeptide
3	1273	99.5	233	22 AAU98014	Human dendritic ce
4	1267	99.0	243	22 AAU98014	Human novel extrac
5	1267	99.0	243	23 ABP48034	Human polypeptide
6	1267	99.0	246	22 AAU19653	Human polypeptide
7	1267	99.0	246	22 ABP48773	Human novel extrac
8	1059.5	82.8	198	23 ABP63043	Human polypeptide
9	672.5	52.5	238	20 AAW88128	Rodent DCMPI C-1ec

10	552	43.1	211	22 AAE12080	Dendritic cell (DC
11	551.5	43.1	213	22 AAB84215	Amino acid sequenc
12	551.5	43.1	213	22 AAE27987	Human dectin prote
13	551.5	43.1	218	22 AAE12079	Dendritic cell (DC
14	534.5	41.8	182	23 AAE27988	Human dectin prote
15	507.5	39.6	134	23 AAU98013	Human partial dend
16	507.5	39.6	148	23 AAU98015	Human partial dend
17	489	38.2	209	19 AAW63010	Mouse dectin-2, M
18	489	38.2	209	22 AAY27447	Mouse SDCMP3 poly
19	489	38.2	209	22 AAW00482	Mouse dectin-2 ext
20	473.5	37.0	167	19 AAW63022	Mouse dectin-2 ext
21	458	35.8	209	22 AAU00479	Human TANGO 405 pr
22	452.5	35.4	145	19 AAW63017	Mouse dectin-2 iso
23	452.5	35.4	175	19 AAW63018	Mouse dectin-2 iso
24	356	27.8	59	23 ABE80759	C-type lectin-like
25	335.5	26.2	162	20 AAY27446	Human SDCMP3 poly
26	330.5	25.8	168	19 AAW63020	Mouse dectin-2 iso
27	330	25.8	219	20 AAY13403	Amino acid sequenc
28	330	25.8	219	22 AAU29035	Human PRO polypept
29	330	25.8	219	22 AAB74697	Human membrane ass
30	330	25.8	219	22 AAB80271	Human PRO244 prote
31	330	25.8	219	24 ABO69681	Novel human secret
32	330	25.8	219	24 ABO71123	Human PRO244 prote
33	330	25.8	219	24 ABO71504	Human PRO polypept
34	330	25.8	219	24 ABO71950	Human secreted/ltra
35	330	25.8	219	24 ABO65580	Human secreted/ltra
36	330	25.8	219	24 ABO65913	Novel human secret
37	330	25.8	219	24 ABO67404	Human secreted pro
38	330	25.8	219	24 ABO67417	Human secreted/ltra
39	330	25.8	219	24 ABO64558	Human secreted/ltra
40	330	25.8	219	24 ABO65275	Human PRO polypept
41	330	25.8	219	24 ABO58411	Human PRO polypept
42	330	25.8	219	24 ABO55947	Human secreted/ltra
43	330	25.8	219	24 ABO56942	Human PRO polypept
44	330	25.8	219	24 ABO58406	Human secreted/ltra
45	330	25.8	219	24 ABO10521	Human secreted/ltra

ALIGNMENTS

RESULT 1	
AAW88124	AAW88124 standard; Protein; 237 AA.
ID	AAW88124;
AC	AAW88124;
XX	
DT	11-MAY-1999 (first entry)
DE	Primate DCMPI C-1e lectin family gene protein sequence.
XX	
KW	Primate: dendritic cell membrane protein; DCMPI; DCMPI;
KW	Chromosomal abnormality; expression misregulation;
KW	abnormal proliferation; regeneration; degeneration; haematopoietic cell.
OS	Mammalia.
XX	
PN	WO9902562-A1.
XX	
PD	21-JAN-1999.
XX	
PF	08-JUL-1998; 98MO-US13436.
XX	
PR	09-JUL-1997; 97US-0053080.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Bates EM, Ford J, Lebecque SE, Ravel O, Saeland S;
XX	Valladeau J;
DR	WPI: 1999-120786/10.
XX	N-PSDB; AAX04865.
XX	

PT Dendritic cell membrane proteins - used to treat conditions
PT associated with abnormal physiology or development
XX
PS Claim 1; Page 65-66; 82pp; English.
XX
CC Dendritic cell membrane protein 1 (DCMP1) and DCMP2 nucleic acids can be
CC used as markers for distinguishing cell types, including genomic aspects
CC of cells, as well as mRNA and protein expression patterns. They can also
CC be used to detect chromosomal abnormalities. The proteins can be used to
CC diagnose disorders associated with expression misregulation. They can
CC also be used to treat conditions associated with abnormal physiology or
CC development, including abnormal proliferation, e.g. cancerous conditions
CC or degenerative conditions. Abnormal proliferation, regeneration,
CC degeneration and atrophy may be modulated using the proteins. The
CC proteins may also play a role in regulation or development of
CC hematopoietic cells.
XX
SQ Sequence 237 AA;
XX
Query Match 100.0%; Score 1280; DB 20; Length 237;
Best Local Similarity 100.0%; Pred. No. 6.7e-127;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MTSKITAEVRFNFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFPELLAIS 60
Db 1 MTSKITAEVRFNFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFPELLAIS 60
QY 61 FFLAFVFFQKYSQLEKTKTKELVHTTLCVKKNMPEETANSCCPKNNKSSSNCFI 120
Db 61 FFLAFVFFQKYSQLEKTKTKELVHTTLCVKKNMPEETANSCCPKNNKSSSNCFI 120
QY 121 STESASWQSEKOCARMEAHLLVINTQEBODFIQONQESAFVGLSDPEGORHQMWD 180
Db 121 STESASWQSEKOCARMEAHLLVINTQEBODFIQONQESAFVGLSDPEGORHQMWD 180
QY 181 QTPYNESSTFWHPRESDPNERCYVILNFRKSPKRWGNDVNCIGPORSVCEMMKIH 237
Db 181 QTPYNESSTFWHPRESDPNERCYVILNFRKSPKRWGNDVNCIGPORSVCEMMKIH 237
XX
RESULT 2
AB90277
ID ABB90277 standard; Protein: 237 AA.
XX
AC ABB90277;
XX
24-MAY-2002 (first entry)
XX
Human polypeptide SEQ ID NO 2653.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vlnnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
XX
N-PSDB; ABL90686.

PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX
PS Claim 11; SEQ ID NO 2653; 2081pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABL9449-ABL90853) and proteins
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at http://wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 237 AA;
XX
Query Match 99.6%; Score 1275; DB 23; Length 237;
Best Local Similarity 99.6%; Pred. No. 2.3e-126;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MTSKITAEVRFNFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFPELLAIS 60
Db 1 MTSKITAEVRFNFKSSGINTASSAASKERTAPLKSNTGFPKLLCASLIFPELLAIS 60
QY 61 FFLAFVFFQKYSQLEKTKTKELVHTTLCVKKNMPEETANSCCPKNNKSSSNCFI 120
Db 61 FFLAFVFFQKYSQLEKTKTKELVHTTLCVKKNMPEETANSCCPKNNKSSSNCFI 120
QY 121 STESASWQSEKOCARMEAHLLVINTQEBODFIQONQESAFVGLSDPEGORHQMWD 180
Db 121 STESASWQSEKOCARMEAHLLVINTQEBODFIQONQESAFVGLSDPEGORHQMWD 180
QY 181 QTPYNESSTFWHPRESDPNERCYVILNFRKSPKRWGNDVNCIGPORSVCEMMKIH 237
Db 181 QTPYNESSTFWHPRESDPNERCYVILNFRKSPKRWGNDVNCIGPORSVCEMMKIH 237
XX
RESULT 3
AAU98014
ID AAU98014 standard; Protein: 237 AA.
XX
AC AAU98014;
XX
27-AUG-2002 (first entry)
XX
Human dendritic cell immunoreceptor AU133532.
XX
XX Human: dendritic cell immunoreceptor; cytostatic;
KW antiasthmatic; anorectic; antidiabetic; cancer; allergy; anaphylaxis;
KW asthma; inflammation; obesity; diabetes; central nervous system disorder;
KW Alzheimer's disease; Parkinson's disease; dementia; osteoarthritis;
KW cardiovascular disorder; myocardial infarction; ischemic heart disease;
KW congestive heart failure; chronic obstructive pulmonary disease; COPD.
XX
OS Homo sapiens.
XX
PN WO200232958-A2.
XX
PD 25-APR-2002.
XX
PF 12-OCT-2001; 2001WO-EP11812.

PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0238935.
PR 13-OCT-2000; 2000US-0238937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-465572/50.
DR N-PSDB; AAS31385.
XX
PT Nucleic acid molecules encoding human secreted extracellular matrix
PT proteins, used in preventing, treating or ameliorating a disorder, e.g.
PT Alzheimer's and Parkinson's diseases and cancers -
XX
PS Claim 11; SEQ ID No 464; 577bp; English.
XX
CC The invention relates to isolated nucleic acid molecules encoding
CC novel human secreted extracellular matrix proteins (SPs). The
CC polynucleotides and proteins are used to prevent, treat a medical
CC condition in e.g. humans, mice, rabbits, goats, cats, dogs,
CC chickens or sheep. For example, disorders associated with decreased
CC expression of SPs. The SP polynucleotide or a vector expressing them may
CC be administered to treat diseases by gene therapy. Antisense molecules
CC may be administered to down regulate expression of SPs by binding with
CC the cells own genes and preventing their expression. The polynucleotides
CC may also be used as DNA probes in diagnostic assays. The SPs may also be
CC used as antigens to produce antibodies and to identify modulators
CC (agonists and antagonists) of the SPs. The anti-(SP) antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC SP and as diagnostic agents for detecting the presence of SPs in samples.
CC The disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac
CC arrest, tachycardia and angina), infections caused by bacteria, viruses
CC and fungi and ocular disorders (e.g. corneal infections). Other uses
CC include wound healing, maintenance of organs before transplantation,
Query Match 99.0%; Score 1267; DB 22; Length 243;
Best Local Similarity 99.6%; Pred No. 1.6e-125;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 SEITAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGFPRLCALSILIFLLAISFF 62
DB :|||||
9 AEITAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGFPRLCALSILIFLLAISFF 68
QY 63 IAFVIFPQKYSOLLEKTKTKELVHTTLEEVKKNMVEEERAWSCCRKNKSSFNCTYFST 122
DB :|||||
69 IAFVIFPQKYSOLLEKTKTKELVHTTLEEVKKNMVEEERAWSCCRKNKSSFNCTYFST 128
QY 123 ESASMODSEKDCARMEAHLLVINTOEEDOFICONTLOESASVYVGSDEPGQRHMQVQOT 182
DB :|||||
129 ESASMODSEKDCARMEAHLLVINTOEEDOFICONTLOESASVYVGSDEPGQRHMQVQOT 188
QY 183 PYNESSTFWHPREPSDPNERCVVLFRRSPKRMGNNDVNCGLPORSVCEMMKIH 237
DB :|||||
189 PYNESSTFWHPREPSDPNERCVVLFRRSPKRMGNNDVNCGLPORSVCEMMKIH 243
RESULT 5
ABP48034
ID ABP48034 standard; Protein; 243 AA.
XX
AC ABP48034;
XX

DT 23-AUG-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 464.
XX
KW Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnereary;
KW antiparkinsonian; antischistosomal; antitubercular; cancer;
KW antirheumatic; hepatoprotective; cerebroprotective; anti-inflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US2002042386-A1.
XX
PD 11-APR-2002.
XX
PF 17-JAN-2001; 2001US-0764870.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214866P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216680P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225477P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226688P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 13-OCT-2000; 2000US-237040P.
PR 20-OCT-2000; 2000US-239935P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
XX
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.
XX
XX
PI Rosen CA, Ruben SM, Barash SC.
XX
XX
DR WPI: 2002-470713/50.
XX
XX N-PSDB: AB066709.
PT New nucleic acid encoding human proteins, useful for diagnosis,
PT treatment and prevention of e.g. osteoporosis, also related
XX polypeptides and antibodies
XX
PS Claim 11; SEQ ID NO 464; 235pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AB066521-AB066765) and proteins
CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?docID=999909764870.
XX
SQ Sequence 243 AA:

Query Match 99.0%; Score 1267; DB 23; Length 243;
Best local similarity 99.6%; Pred. No. 1.6e-125;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEITTAEVKFKNEFSSGINTASSAASKRTAPLKSNTGPKLLCASLIFLLAISFF 62
DB :|||||
DB 9 AEITTAEVKFKNEFSSGINTASSAASKRTAPLKSNTGPKLLCASLIFLLAISFF 68
QY 63 IAFVIFFOKYSOLLEKTKTKELVHTLECVKNNMPEETAWSCCPKNNKSFSSNCYFIST 122
DB :|||||
DB 69 IAFVIFFOKYSOLLEKTKTKELVHTLECVKNNMPEETAWSCCPKNNKSFSSNCYFIST 128
QY 123 ESASWDSKDCARNEAHLVINTOEODFIFONTLOESAYVEVGLSDPGQRHMQVDDT 182
DB :|||||
DB 129 ESASWDSKDCARNEAHLVINTOEODFIFONTLOESAYVEVGLSDPGQRHMQVDDT 188
QY 183 PYNESSTFWHPRESDPNERCVVNLNFKSPKRWGNDVNCCLPQNSVCMMKITHL 237
DB :|||||
DB 189 PYNESSTFWHPRESDPNERCVVNLNFKSPKRWGNDVNCCLPQNSVCMMKITHL 243

RESULT 6.
AAU19653
ID AAU19653 standard; Protein: 246 AA.
XX
XX AAU19653;
AC
XX
DT 04-DEC-2001 (first entry)
XX
XX
DE Human novel extracellular matrix protein, Seq ID No 303.
XX
XX
KW Human; secreted extracellular matrix protein; immunomodulatory;
KW Anti-HIV; antianemic; antirheumatic; antischistosomal; cardiac; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytosolic;
KW antiallergic; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;
KW Sezary syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;

KM cardiac arrest; tachycardia; angina; infection; corneal infections;
 XX wound healing; immunogen; gene therapy; antisense; food additive.
 OS Homo sapiens.
 XX WO200155368-A1.
 PN 02-AUG-2001.
 XX 17-JAN-2001; 2001WO-US01348.
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216680.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226686.
 PR 22-AUG-2000; 2000US-0227182.
 PR 22-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
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 PR 05-SEP-2000; 2000US-0229513.
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 PR 06-SEP-2000; 2000US-0230438.
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 PR 08-SEP-2000; 2000US-0231243.
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 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
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PR 25-SEP-2000; 2000US-0234997.
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 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
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 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
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 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.

PT New nucleic acid encoding human proteins, useful for diagnosis,
 PT treatment and prevention of e.g. osteoporosis, also related
 PT polypeptides and antibodies
 PS Claim 11; SEQ ID NO 303; 235pp + Sequence Listing; English.

XX The invention relates to novel genes (AB066521-AB066785) and proteins
 CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html?docID=999909764870.

XX Sequence 246 AA:

Query Match 99.0%; Score 1267; DB 23; Length 246;
 Best Local Similarity 99.6%; Pred. No. 1.7e-125;
 Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEITTAEVRRKNEFKSSGINTASSASKERTAPLKSNTGPKLLCASLIFLLAISFF 62
 DB 12 ABITTAEVRRKNEFKSSGINTASSASKERTAPLKSNTGPKLLCASLIFLLAISFF 71
 QY 63 IAFVIFFOKYSQLEKKTKELVHTTLECYKKNMPVEETAMSCCPKMKKSFSSNCFIT 122
 DB 72 IAFVIFFOKYSQLEKKTKELVHTTLECYKKNMPVEETAMSCCPKMKKSFSSNCFIT 131
 QY 123 ESASMODSEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORHOMVDT 182
 DB 132 ESASMODSEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORHOMVDT 191
 QY 183 PYNESSTFWHPRPSDPNERCVVLFNFKSPKRMGMDVNCIGPORSVCCEMKIHL 237
 DB 192 PYNESSTFWHPRPSDPNERCVVLFNFKSPKRMGMDVNCIGPORSVCCEMKIHL 246

RESULT 8
 APP63043
 ID APP63043 standard; Protein; 198 AA.
 XX
 AC APP63043;
 XX
 DT 14-OCT-2002 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 480.
 XX
 KW Human; vulnereary; dermatological; neuroprotective; nootropic; cancer;
 KW antiparkinsonian; immunostimulant; cyostatic; immunosuppressive;
 KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
 KW burn; central nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; immune disorder;
 KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200218424-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-US27093.
 XX

PR 01-SEP-2000; 2000US-0654935.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
 DR WPI: 2002-583321/62.
 DR N-PDSB; AB093522.
 XX
 PT New polynucleotide and polypeptides, useful for treatment and diagnosis
 PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
 PT sclerosis, diabetes and allergies -
 PS Claim 20; SEQ ID NO 480; 284pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (i) comprising one of
 CC 245 sequences (AB093288-AB093532). Treating a condition comprising
 CC administering to a mammalian subject a composition comprising the protein
 CC (II) encoded by (i) (ABP62809-ABP63053) or an antibody (III) to (II).
 CC (i) (i) and (iii) are useful for diagnostic evaluation of disorders.
 CC (ii) is useful for gene therapy of diseases and (iii) can be used for
 CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

XX Sequence 198 AA:

Query Match 82.8%; Score 1059.5; DB 23; Length 198;
 Best Local Similarity 83.1%; Pred. No. 1.1e-103;
 Matches 197; Conservative 1; Mismatches 0; Indels 39; Gaps 1;

QY 1 MTSEITTAEVRRKNEFKSSGINTASSASKERTAPLKSNTGPKLLCASLIFLLAIS 60
 DB 1 MISEITTAEVRRKNEFKSSGINTASSA----- 27
 QY 61 FPIAIVIFFOKYSQLEKKTKELVHTTLECYKKNMPVEETAMSCCPKMKKSFSSNCFIT 120
 DB 28 -----VFQKYSQLEKKTKELVHTTLECYKKNMPVEETAMSCCPKMKKSFSSNCFIT 81
 QY 121 STESASMODSEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORHOMVDT 180
 DB 82 STESASMODSEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORHOMVDT 141
 QY 181 QTPYNESSTFWHPRPSDPNERCVVLFNFKSPKRMGMDVNCIGPORSVCCEMKIHL 237
 DB 142 QTPYNESSTFWHPRPSDPNERCVVLFNFKSPKRMGMDVNCIGPORSVCCEMKIHL 198

RESULT 9
 AAW88128
 ID AAW88128 standard; Protein; 238 AA.
 XX
 AC AAW88128;
 XX
 DT 11-MAY-1999 (first entry)
 XX
 DE Rodent DCMPI C-lectin family gene protein sequence.
 XX
 KW Rodent; dendritic cell membrane protein; DCMPI; DCMPI2;
 KW chromosomal abnormality; expression misregulation;
 KW abnormal proliferation; regeneration; degeneration; hematopoietic cell.
 XX
 OS Mammalia.
 XX
 PN WO9902562-A1.
 XX

PD 21-JAN-1999.
 XX 08-JUL-1998; 98WO-US13436.
 PF 09-JUL-1997; 97US-0053080.
 PR (SCHE) SCHERING CORP.
 XX
 PA Bates EEM, Ford J, Lebecque SJE, Ravel O, Saeland S;
 PI Valladeau J;
 DR WPI: 1999-120786/10.
 N-PSDB: AAX04867.
 XX
 XX Dendritic cell membrane proteins - used to treat conditions
 PT associated with abnormal physiology or development
 XX
 PS Claim 1; Page 73-75; 82pp; English.
 CC Dendritic cell membrane protein 1 (DCMP1) and DCMP2 nucleic acids can be
 CC used as markers for distinguishing cell types, including genomic aspects
 CC of cells, as well as mRNA and protein expression patterns. They can also
 CC be used to detect chromosomal abnormalities. The proteins can be used to
 CC diagnose disorders associated with expression misregulation. They can
 CC also be used to treat conditions associated with abnormal physiology or
 CC development, including abnormal proliferation, e.g. cancerous conditions
 CC or degenerative conditions. Abnormal proliferation, regeneration,
 CC degeneration and atrophy may be modulated using the proteins. The
 CC proteins may also play a role in regulation or development of
 CC haematopoietic cells.
 CC
 XX Sequence 238 AA;
 SO

Query Match 52.5%; Score 672.5; DB 20; Length 238;
 Best Local Similarity 53.3%; Pred. No. 1.3e-62;
 Matches 129; Conservative 37; Mismatches 67; Indels 9; Gaps 6;

OY 1 MTSETTYAEVRFKFKSSGINTASSAASKERTAPLKS--NTGPKLCASLIFFLILA 58
 DB 1 MASETTYAEVRFKNE--SNSLHTYSESPAAREKPIRLKRGSSLLTSLMLLLILA 58
 OY 59 ISFTIAYEIVFQKTSQLL-EKKTKELVHTLIECVKKNMPYETAWSCCPKRWKSSSNC 117
 DB 1 ITFLVAFIIFQKTSQLL-EKKTKELVHTLIECVKKNMPYETAWSCCPKRWKSSSNC 117
 OY 118 YFIST--ESASMOSEKDCARMEHLLVINTQEDDTFQNLQESATFVGLSPDEGRH 175
 DB 119 YLVPVSSSSASWMSSEKSRGALVLIQSOEDDTFTGLDTHAAVFIQLMD-TGHRQ 177
 OY 176 WQWVDQPTNYSSTFWHREPSDNERCVLNFKSPKRWGMNDVNCGPQSRVCEMKKI 235
 DB 178 WQWVDQPTNYSSTFWHREPSDNERCVLNFKSPKRWGMNDVNCGPQSRVCEMKKI 235
 OY 236 HL 237
 DB 237 NL 238
 RESULT 10
 AAEL2080
 ID AAEL2080 standard; Protein; 211 AA.
 XX
 AC AAEL2080;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 XX Dendritic cell (DC) DCLEC/SPLICE 1 variant protein.
 DE
 XX Dendritic cell; DC; DCLEC protein; gene therapy; dermatological; vaccine;
 KW atopic dermatitis; autoimmune disease; inflammatory skin disease; cancer;
 KW immunosuppressive; AIDS; Acquired immune deficiency syndrome; cytotoxic;
 KW chromosomal identification; pharmaceutical; hypersensitivity; virucide;
 KW transplant rejection; chronic inflammatory disease; anti-HIV; variant.

XX Unidentified.
 OS Location/Qualifiers
 XX Key
 FH Misc-difference 1
 FT /note= "Encoded by C"
 FT
 PN W020012773-A2.
 XX
 PD 04-OCT-2001.
 XX
 PD 28-MAR-2001; 2001WO-EP03542.
 PF
 XX 29-MAR-2000; 2000US-192934P.
 PR 18-MAY-2000; 2000US-205020P.
 PR 18-MAY-2000; 2000US-205026P.
 PR 19-MAY-2000; 2000US-205767P.
 PR 19-MAY-2000; 2000US-205769P.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Werner G, Phares W, Jarlitz M, Lapp H, Kalthoff FS;
 XX
 DR WPI: 2001-616466/71.
 N-PSDB: AAD19730.
 XX
 PT New polypeptides for screening therapeutic agonists and antagonists
 PT comprise dendritic cell polypeptides
 XX
 PS Claim 2; Page 52; 52pp; English.
 XX

The invention relates to dendritic cell (DC) proteins and their
 CC corresponding DNA molecules. A pharmaceutical composition comprising
 CC agonist and antagonist of DC proteins are useful for treating abnormal
 CC conditions related to both an excess of and insufficient level of
 CC expression of DC gene, or related to both an excess of and insufficient
 CC activity of DC protein. Soluble form of DC proteins are used as an active
 CC ingredient in combination with pharmaceutical acceptable carriers.
 CC DC genes and proteins are useful for treating chronic inflammatory
 CC diseases, autoimmune diseases, transplant rejection crisis, including
 CC inflammatory skin diseases such as contact hypersensitivity, atopic
 CC dermatitis or virally-induced immune suppression such as AIDS and cancer.
 CC DC protein is useful for inducing immunological response in a mammal, and
 CC as immunogen to produce antibodies immunospecific for the polypeptide.
 CC DC gene is useful in gene therapy. DC gene is also useful as a diagnostic
 CC reagent, and for chromosomal identification. The present sequence is
 CC dendritic cell (DC) DCLEC/SPLICE 1 variant protein which is found to
 CC belong to the family of C-type lectins with one single carbohydrate
 CC recognition domain at the C-terminal end.
 SO

Query Match 43.1%; Score 552; DB 22; Length 211;
 Best Local Similarity 47.7%; Pred. No. 6.1e-50;
 Matches 102; Conservative 42; Mismatches 60; Indels 10; Gaps 4;

OY 28 ASKERTAPLKSNTGPKLCASLIFFLILAISFTIAYT----FQKYSQLEKKTKE 83
 DB 4 ASEDRE--KGLMFWOLKWSMAVAYSTLLSVCFVSSVPHNMYSTVRLSLREYQ 60
 OY 84 LVHTTLECVKKNMPYETAWSCCPKRWKSSSNCYFISTESASMODSEKDCARMEHLLV 143
 DB 61 QYHPSLTVMGCKDIED--WSCCPPTWTSFSSCTFISTGMSWTKSKNCSYMGADLV 118
 OY 144 INTQEDDTFQNLQESATFVGLSPDEGRHWMQWVDQPTNYSSTFWHREPSDNERC 203
 DB 119 INTREEDQPTIIONLKRNSYFLGLSDPGRRHWMQWVDQPTNENVTFWHSGEPNNLDERC 178
 OY 204 VLVNFRKSPKRWGMNDVNCLOPQSRVCEMKKIHL 237
 DB 179 AINFRSS-EEGMNDHICHVPOKRSICKMKKIYI 211

XX	AAE12079;	
AC		
XX		
XX	18-DEC-2001	(first entry)
DT		
XX		
DE	Dendritic cell (DC)	DCLEC protein.
XX		
KW	Dendritic cell; DC; DCLEC protein; gene therapy; dermatological; vaccine;	
KW	atopic dermatitis; autoimmune disease; inflammatory skin disease; cancer;	
KW	immunosuppressive; AIDS; Acquired immune deficiency syndrome; cytostatic;	
KW	chromosomal identification; pharmaceutical; hypersensitivity; virucide;	
KW	transplant rejection; chronic inflammatory disease; anti-HIV.	
XX		
OS	unidentified.	
XX		
XX		
FH	Key	Location/Qualifiers
FT	Domain	26..46
FT		/note= "Single transmembrane region"
FT	Domain	114..211
FT		/note= "Extracellular C-type lectin domain"
XX		

04-OCT-2001.

28-MAR-2001; 2001WO-EP03542.

XX 29-MAR-2000; 2000US-192934P
PR 18-MAY-2000; 2000US-205020P
PR 18-MAY-2000; 2000US-205026P
PR 19-MAY-2000; 2000US-205767P
PR 19-MAY-2000; 2000US-205769P

PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH

PI. Werner G, Phares W, Jaritz M, Lapp H, Kalthoff FS;

DR WPI; 2001-616466/71.
DR N-PSDB; AAD19729.

PT New polypeptides for screening therapeutic agonists and antagonists
PT comprise dendritic cell polypeptides -
XX
PS Claim 2, Page 51, 52pp; English.

The invention relates to dendritic cell (DC) proteins and their corresponding DNA molecules. A pharmaceutical composition comprising agonist and antagonist of DC proteins are useful for treating abnormal conditions related to both an excess of and insufficient level of expression of DC gene, or related to both an excess of and insufficient activity of DC protein. Soluble form of DC proteins are used as an active ingredient in combination with pharmaceutical acceptable carriers. DC genes and proteins are useful for treating chronic inflammatory diseases, autoimmune diseases, transplant rejection crisis, including inflammatory skin diseases such as contact hypersensitivity, atopic dermatitis or virally-induced immune suppression such as AIDS and cancer. DC protein is useful for inducing immunosuppression in a mammal, and as immunogen to produce antibodies immunospecific for the polypeptide. DC gene is useful in gene therapy. DC gene is also useful as a diagnostic reagent, and for chromosomal identification. The present sequence is dendritic cell (DC) DCLE protein identification. The present sequence is of C-type lectins with one single carbohydrate recognition domain at the C-terminal end.

SQ Sequence 218 AA;

Query Match	Score	DB	Length
43.18;	551.5;	DB 22;	Length 218;

Matches 97; Conservative 38; Mismatches 49; Indels 7; Gaps 3;

```

0Y      51. LIFELLALSFIAFVI----FFQKXSÖLEKKTTELVTHTTECYAKNMPDETANSCC 106
       :: ||:: | :: | : | : | : | : | : | : | : | : | : | : | : | : |

```

Db	3	VSEILLLSVGFVYSSVVPHPNFMYKTVKRLSLRLREYQYHPSLCLVMEGKNIED--	-NSCC	88
QY	107	PKMKSFSSNCYITISTESASMODSEKDCARMEAHLLVINTQBEDFTFQNLQEEASAYFVG	166	
Db	89	PTFMTSFQSSCYITISTGMSQWTKRSQKNCSVMGADLVVINTREEDFTFIQNLKRNSSYFLG	148	
QY	167	LSDPDEGRHMQWQDQFPYNESSTFMHRRSPSDNRCVYVLMFRKSPKRWGKNVDVNCGLPQ	226	
Db	149	LSDPGGGRHMQWQDQFPYNEENVTFWHSGEPPNLDLRCALINFRSS--EEMGNWDDHCHVPQ	207	
QY	227	RSVCEMKRIHL	237	
Db	208	KSICKMKKIYI	218	

RESULT 14
AAE27988
ID AAE27988 standard; Protein; 182 AA

AC AAE27988;

DT 27-JAN-2003 (first entry)

Human dectin protein #2.

KW Human; dectin; novel human protein; NHP; gene therapy; cancer; arthritis;
inflammatory disorder; infection; cytostatic; antibacterial.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	Misc-difference, 35	

/note= "Xaa corresponds to any amino acid;
Encoded by YCA"

PN WO200272603-A2.

PD. 19-SEP-2002

PF 01-MAR-2002; 2002WO-US06711.

PR 12-MAR-2001; 2001US-274961P.

PA (LEXI-) LEXICON GENETICS INC.

PI Turner CA, Mathur B, Cullinan EB;

DR WPI; 2002-723313/78.

XX
X
.
. .
- - - - -

PT treating disorders associated with aberrant NHP expression and

PT infection -

PS Claim 4; Page 36-37; 37pp; English.

CC The present sequence is dectin protein, a novel human protein

CC as hybridisation probes for screening libraries. The compositions and

CC treating disorders associated with aberrant NHP expression and activity,

33 XX

[illegible]

Best Local Similarity 54.48; Pred. NO. 3.6e-48;

[illegible]

06 : | : | : | : | : | : | : | : | : | : | : | : | : |

17 VCEWVDF CWT DEVOOVYCT ECVMECREDTD - ESOCODTHWCESOCSCVEYECMCVCUVM 74

QY 129 DSEKDCARMEAHLLVINTQEDPFIQNLQESAYFVGLSDPEGGRHQMWDQTPYNSS 188
 Db 75 KSKKNCYWGADLVYINTREEDFIQNLKRNSYFGLSDPEGGRHQMWDQTPYNENV 134
 QY 189 TFWHRESDNERECVYNFRKSPKRGANDVNCIGPORSCEMKKIHL 237
 Db 135 TFWHSGEPNNLDERCAIINFRSS-BEWMNDIHCHVPOKSIKMKKIYI 182

RESULT 15
 AAU98013
 ID AAU98013 standard; Protein; 134 AA.
 AC AAU98013;
 XX
 DT 27-AUG-2002 (first entry)
 XX

Human partial dendritic cell immunoreceptor #1.

KW Human; dendritic cell immunoreceptor; cytostatic;
 KW antihistaminic; anorectic; antidiabetic; cancer; allergy; anaphylaxis;
 KW asthma; inflammation; obesity; diabetes; central nervous system disorder;
 KW Alzheimer's disease; Parkinson's disease; dementia; osteoarthritis;
 KW cardiovascular disorder; myocardial infarction; ischaemic heart disease;
 KW congestive heart failure; chronic obstructive pulmonary disease; COPD.
 XX
 OS Homo sapiens.
 XX
 PN MO200232958-A2.
 PD 25-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-EP11812.
 XX
 PR 16-OCT-2000; 2000US-240096P.
 PR 27-AUG-2001; 2001US-314661P.
 XX
 PA (PARB) BAYER AG.
 XX
 PI Smolylar A;
 XX
 DR WPI: 2002-463308/49.
 DR N-PSDB; ABR52903.
 XX

Novel human dendritic cell immunoreceptor polypeptide, useful for treating cancer, asthma, obesity, diabetes, central nervous system disorder or cardiovascular disorder

Claim 25; Fig 2; 114pp; English.

The invention relates to a purified human dendritic cell immunoreceptor polypeptide and its encoding nucleic acid. Also included are an expression vector comprising the nucleic acid, a host cell containing the vector, reducing the activity of human dendritic cell immunoreceptor involves contacting a cell with a reagent which specifically binds to the polypeptide or nucleic acid and a reagent that modulates the activity of the polypeptide or nucleic acid. The reagent is useful for the preparation of a medicament for modulating the activity of human dendritic cell immunoreceptor in a disease such as cancer, allergy, anaphylaxis, asthma, inflammation, obesity, diabetes, a central nervous system (CNS) disorder (e.g. Alzheimer's disease, Parkinson's disease or dementia), or a cardiovascular disorder (e.g. myocardial infarction, ischaemic heart disease, congestive heart failure), chronic obstructive pulmonary disease (COPD) and osteoarthritis (many other diseases and disorders are listed in the specification). The polypeptide and nucleic acid are useful for identifying test compounds which act as agonists or antagonists, for raising specific antibodies, and as a bait protein in a two-hybrid or three-hybrid assay. The nucleic acid is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to disease and abnormalities related to the presence of mutations. The present sequence represents a partial sequence of a dendritic cell immunoreceptor.

XX
 SQ Sequence 134 AA;
 Query Match 39.6%; Score 507.5; DB 23; Length 134;
 Best Local Similarity 62.2%; Pred. No. 1.7e-45;
 Matches 84; Conservative 24; Mismatches 26; Indels 1; Gaps 1;

QY 103 WSCCPKNNKSFSSNCFYFISTESASWQSEKDCARMEAHLLVINTQEDPFIQNLQESAY 162
 Db 1 MSCCPTPMTSPFSSCYFISTGMQSWTKGKNCYWGADLVYINTREEDFIQNLKRNS 60
 QY 163 YFVGLSDPEGGRHQMWDQTPYNESSTFWHRESDNERECVYNFRKSPKRGANDVNC 222
 Db 61 YFGLSDPEGGRHQMWDQTPYNENVTFWHSGEPNNLDERCAIINFRSS-BEWMNDIHCH 119
 QY 223 LGPORSCEMKKIHL 237
 Db 120 HYPKSIKMKKIYI 134

Search completed: August 4, 2003, 13:08:38
 Job time : 87 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 13:07:18 ; Search time 30 Seconds
(without alignments)
334.256 Million cell updates/sec

Title: US-09-862-802-2

Perfect score: 1280
Sequence: 1 MTSEITYAEVFRKNEKSSG.....NDVNCGLQPSRVCENMKIHL 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	3	US-09-111-470-2
2	672.5	52.5	238	3	US-09-111-470-8
3	489	38.2	209	3	US-08-772-440-4
4	473.5	37.0	167	3	US-08-772-440-21
5	452.5	35.4	145	3	US-08-772-440-14
6	452.5	35.4	175	3	US-08-772-440-15
7	427.5	33.4	131	3	US-08-772-440-23
8	427.5	33.4	131	3	US-08-772-440-27
9	330.5	25.8	168	3	US-08-772-440-17
10	325	25.4	134	3	US-08-772-440-16
11	277.5	21.7	149	4	US-09-489-847-167
12	266.5	20.0	273	3	US-09-111-470-10
13	256.5	20.0	292	2	US-08-688-342-4
14	256.5	20.0	292	2	US-09-113-788-4
15	253	19.8	316	3	US-09-111-470-4
16	240	18.8	85	3	US-08-772-440-32
17	238	18.6	87	4	US-09-489-847-236
18	226	17.7	287	4	US-09-111-470-6
19	220.5	17.2	291	2	US-08-688-342-5
20	220.5	17.2	291	2	US-09-113-788-5
21	220.5	17.2	291	3	US-09-111-470-5
22	218.5	17.1	75	3	US-09-111-470-11
23	212.5	16.6	129	3	US-08-722-126A-10
24	212.5	16.6	129	5	PCT-US95-04258-10
25	210	16.4	272	1	US-08-690-095-1
26	210	16.4	272	3	US-09-113-789-1
27	208.5	16.3	287	1	US-08-365-103B-4

28	208.5	16.3	300	1	US-08-365-103B-6	Sequence 6, Appl
29	208.5	16.3	327	1	US-08-365-103B-2	Sequence 2, Appl
30	207	16.2	1479	3	US-08-840-062-2	Sequence 2, Appl
31	205.5	16.1	404	4	US-09-517-605-2	Sequence 4, Appl
32	204	15.9	1479	3	US-08-840-062-4	Sequence 7, Appl
33	196.5	15.4	125	5	US-08-722-126A-7	Sequence 7, Appl
34	196.5	15.4	125	5	PCT-US95-04258-7	Sequence 17, Appl
35	192.5	15.0	187	4	US-09-535-521-17	Sequence 17, Appl
36	192.5	15.0	208	4	US-09-535-521-20	Sequence 20, Appl
37	192.5	15.0	292	4	US-09-535-521-2	Sequence 5, Appl
38	192.5	15.0	292	4	US-09-535-521-5	Sequence 5, Appl
39	192	15.0	111	6	5514582-11	Patent No. 5514582
40	191	14.9	190	4	US-09-127-946-14	Sequence 14, Appl
41	190	14.8	280	4	US-09-986-243-119	Sequence 19, App
42	188	14.7	123	4	US-09-535-521-25	Sequence 25, Appl
43	188	14.7	128	4	US-09-535-521-8	Sequence 8, Appl
44	188	14.7	139	4	US-09-535-521-11	Sequence 11, Appl
45	188	14.7	141	4	US-09-535-521-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-111-470-2
Sequence 2, Application US/09111470
Patent No. 627959
GENERAL INFORMATION:
APPLICANT: Valladeau, Jenny
APPLICANT: Ravell, Odile
APPLICANT: Bates, Elizabeth E.M.
APPLICANT: Ford, John
APPLICANT: Saeland, Sem
APPLICANT: Lebeque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,470
FILING DATE: 08-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0695
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-111-470-2
Query Match 100.0%; Score 1280; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 6.1e-137;

Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSETIYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGFPKLCASLIFELLAI 60
1 MSETIYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGFPKLCASLIFELLAI 60
Db 1 MSETIYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGFPKLCASLIFELLAI 60

QY 61 FPIAFVIFOKYSQLEKTKTELVHTTECVKKNMVEETAWSCCPKMKSSSNCYFI 120
61 FPIAFVIFOKYSQLEKTKTELVHTTECVKKNMVEETAWSCCPKMKSSSNCYFI 120
Db 61 FPIAFVIFOKYSQLEKTKTELVHTTECVKKNMVEETAWSCCPKMKSSSNCYFI 120

QY 121 STESASWODESKCAREAHLLVINTOEODFIQNLQESAFVGLSDPEGRHQMWD 180
121 STESASWODESKCAREAHLLVINTOEODFIQNLQESAFVGLSDPEGRHQMWD 180
Db 121 STESASWODESKCAREAHLLVINTOEODFIQNLQESAFVGLSDPEGRHQMWD 180

QY 181 QTFYNSSTFWHREPSDNERCVLNFRRSPKRMGMNDVNCIGPQSVCEMMKIH 237
181 QTFYNSSTFWHREPSDNERCVLNFRRSPKRMGMNDVNCIGPQSVCEMMKIH 237
Db 181 QTFYNSSTFWHREPSDNERCVLNFRRSPKRMGMNDVNCIGPQSVCEMMKIH 237

ULT 2
09-111-470-8
; Sequence 8, Application US/09111470
; Patent No. 6277959
; GENERAL INFORMATION:
; APPLICANT: Valladeau, Jenny
; APPLICANT: Ravel, Odile
; APPLICANT: Bates, Elizabeth E.M.
; APPLICANT: Ford, John
; APPLICANT: Saeland, Sem
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Membrane Protein Genes;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,470
; FILING DATE: 08-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,080
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0695
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ. ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-111-470-8

Query Match 52.5%; Score 672.5; DB 3; Length 238;
Best Local Similarity 53.3%; Pred. No. 4.8e-68;
Matches 129; Conservative 37; Mismatches 67; Indels 9; Gaps 6;
QY 1 MSETIYAEVRFKNEKSSGINTASSAASKERTAPLKS--NTGFPKLCASLIFELLAI 58
1 MSETIYAEVRFKNEKSSGINTASSAASKERTAPLKS--NTGFPKLCASLIFELLAI 58

Db 1 MSETIYAEVRFKNE--SNSLHTYSESPAAREKPIRDIJKDPSPLLTSLMLLLIA 58

QY 59 ISFPIAFVIFOKYSQLEKTKTELVHTTECVKKNMVEETAWSCCPKMKSSSNC 117
59 ISFPIAFVIFOKYSQLEKTKTELVHTTECVKKNMVEETAWSCCPKMKSSSNC 117
Db 59 ISFPIAFVIFOKYSQLEKTKTELVHTTECVKKNMVEETAWSCCPKMKSSSNC 117

QY 118 YFIST--ESASWODESKCAREAHLLVINTOEODFIQNLQESAFVGLSDPEGRH 175
118 YFIST--ESASWODESKCAREAHLLVINTOEODFIQNLQESAFVGLSDPEGRH 175
Db 118 YFIST--ESASWODESKCAREAHLLVINTOEODFIQNLQESAFVGLSDPEGRH 175

QY 176 WQVNDQTPYNESSTFWHREPSDNERCVLNFRRSPKRMGMNDVNCIGPQSVCEMM 235
176 WQVNDQTPYNESSTFWHREPSDNERCVLNFRRSPKRMGMNDVNCIGPQSVCEMM 235
Db 176 WQVNDQTPYNESSTFWHREPSDNERCVLNFRRSPKRMGMNDVNCIGPQSVCEMM 235

QY 236 HL 237
237 NL 238
Db 237 NL 238

RESULT 3
US-08-772-440-4
; Sequence 4, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Arizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ. ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 209 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-772-440-4

Query Match 38.2%; Score 489; DB 3; Length 209;
Best Local Similarity 45.2%; Pred. No. 2.6e-47;
Matches 89; Conservative 35; Mismatches 63; Indels 10; Gaps 3;

QY 46 LCASLIFELLAIISFPIAFVIF-----QKTSQLEKTKTELVHTTECVKKNMVEE 100
46 LCASLIFELLAIISFPIAFVIF-----QKTSQLEKTKTELVHTTECVKKNMVEE 100
Db 18 LMSAAVISMILSTCIASCYVYQFIMDQPSRILEHT---YHSSLTCESEGTWSE 73

QY 101 TAWSCCPKMKSSSNCYFIISTESASWODESKCAREAHLLVINTOEODFIQNLQEE 160
101 TAWSCCPKMKSSSNCYFIISTESASWODESKCAREAHLLVINTOEODFIQNLQEE 160
Db 74 KMGCCPNMKSGSSCYLISIKENKWSISEONCVOGMGHLVYINTEADQNTTQOLNS 133

;; CURRENT APPLICATION NUMBER: US/09/489,847
;; CURRENT FILING DATE: 2000-01-24
;; EARLIER APPLICATION NUMBER: PCT/US99/17130
;; EARLIER FILING DATE: 1999-07-29
;; EARLIER APPLICATION NUMBER: 60/094,657
;; EARLIER FILING DATE: 1998-07-30
;; EARLIER APPLICATION NUMBER: 60/095,486
;; EARLIER FILING DATE: 1998-08-05
;; EARLIER APPLICATION NUMBER: 60/096,319
;; EARLIER FILING DATE: 1998-08-12
;; EARLIER APPLICATION NUMBER: 60/095,454
;; EARLIER FILING DATE: 1998-08-06
;; EARLIER APPLICATION NUMBER: 60/095,455
;; EARLIER FILING DATE: 1998-08-06
;; NUMBER OF SEQ ID NOS: 376
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 167
;; LENGTH: 149
;; TYPE: PRT
;; ORGANISM: Homo sapiens
S-09-489-847-167
Query Match 21.7%; Score 277.5; DB 4; Length 149;
Best Local Similarity 35.2%; Pred. No. 1.5e-23;
Matches 50; Conservative 37; Mismatches 50; Indels 5; Gaps 3;
QY 43 PRLICSL-LIFELLAISEFIAPVIFPORYSOLLEKTKELY-HTTLECVKKNPV-- 98
Db 3 POLIPSVIAVETILLGVCFIASCIVTTHNPSRCKRGTVGKHLHAKKLCIKRKSLS 62
QY 99 -EEIWSGCCPRKNKSFSSNCFYISTESASWDSKDCARAEHLVINTOEODFITONL 157
Db 63 AEGSTWCCPDIWMAFQSNCFYPLTDNKTWAESEKNSGGAHLMTISTAEQNFIIQFL 122
QY 158 QEESAYFVGLSDPEGQRHOMV 179
Db 123 DRIISYFLGLDENAKGQMRV 144
RESULT 12
US-09-111-470-10
; Sequence 10, Application US/09111470
; Patent No. 6277959
; GENERAL INFORMATION:
; APPLICANT: Valladeau, Jenny
; APPLICANT: Ravel, Odile
; APPLICANT: Bates, Elizabeth E.M.
; APPLICANT: Ford, John
; APPLICANT: Saeland, Sem
; TITLE OF INVENTION: Mammalian Membrane Protein Genes;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,470
; FILING DATE: 08-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,080
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:

;; NAME: Ching, Edwin P.
;; REGISTRATION NUMBER: 34,090
;; REFERENCE/DOCKET NUMBER: SF0695
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650)852-9196
;; TELEFAX: (650)496-1200
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 273 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-111-470-10
Query Match 20.0%; Score 256.5; DB 3; Length 273;
Best Local Similarity 36.6%; Pred. No. 8.9e-21;
Matches 63; Conservative 25; Mismatches 63; Indels 21; Gaps 8;
QY 72 YSOLL-EKRTRELHTTLECVKKNPVEE--TAMSCCPKNNKSFSSNCFYISTESASW 127
Db 100 HSEMLTRVQOLVODLKLTCQVATLNNNGEASTEGTCVPVNVHEQDSCYFSSGMSW 159
QY 128 QDSKDCARAEHLVINTOEODFITONQESAY-FVGLSDPEGQRHOMVDPQRYNE 186
Db 160 AEAKRYQLNNAHLVINSREQNFYOKYL--GSATYMWGLSDPEGA--WKWVDGTDYAT 215
QY 187 SSTFWHREPSD-----PNERCVLNFRRKSPKRMGMNDVNCIGPORSYCE 231
Db 216 GFQWNRKGPDDMDGCHGLGGEDCA--HFRPDR--WNDDVQGRPYHWCE 262
RESULT 13
US-08-688-342-4
; Sequence 4, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goll, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: Genbank

CLONE: 1235724
US-08-688-342-4

Query Match 20.0%; Score 256.5; DB 2; Length 292;
Best Local Similarity 36.6%; Pred. No. 9.8e-21;
Matches 63; Conservative 25; Mismatches 63; Indels 21; Gaps 8;

QY 72 YSQL--EKKTKELVHTTECVKKNMPVEE--TAWSCCPKMKSFSSNCYFISTESASW 127
DB 119 HSEMLLRVQQLVQDLKLTCTQVATLNNNGEASTEGTCPPVNVYEHQDSCYWFSGMSW 178
QY 128 QDSKDCARMAHLVINTQEDQFIFONLOESAY-FVGLSDPEGQRHMQWVDTPYNE 186
DB 179 AEAKEYQQLKNAHLVINSREQNFVQKYL--GSATYTMGLSDEGA--WKWVGDTYAT 234
QY 187 SSTFMHREPSD-----PNERCVLNFRRKSPRGMNDVNCIGPORSVCE 231
DB 235 GFQWKKRGPDPDDMOGHGLGGGEDCA--HFHDPGR---WMDVYCORPYHWCE 281

RESULT 14

Sequence 4, Application US/09113788
Patent No. 5969104

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1235724
US-09-113-788-4

Query Match 20.0%; Score 256.5; DB 2; Length 292;
Best Local Similarity 36.6%; Pred. No. 9.8e-21;
Matches 63; Conservative 25; Mismatches 63; Indels 21; Gaps 8;

QY 72 YSQL--EKKTKELVHTTECVKKNMPVEE--TAWSCCPKMKSFSSNCYFISTESASW 127

DB 119 HSEMLLRVQQLVQDLKLTCTQVATLNNNGEASTEGTCPPVNVYEHQDSCYWFSGMSW 178

QY 128 QDSKDCARMAHLVINTQEDQFIFONLOESAY-FVGLSDPEGQRHMQWVDTPYNE 186
DB 179 AEAKEYQQLKNAHLVINSREQNFVQKYL--GSATYTMGLSDEGA--WKWVGDTYAT 234

QY 187 SSTFMHREPSD-----PNERCVLNFRRKSPRGMNDVNCIGPORSVCE 231
DB 235 GFQWKKRGPDPDDMOGHGLGGGEDCA--HFHDPGR---WMDVYCORPYHWCE 281

RESULT 15

Sequence 4, Application US/09111470
Patent No. 627959

GENERAL INFORMATION:

APPLICANT: Valladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth E.M.
APPLICANT: Ford, John
APPLICANT: Saeland, Sem
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,470
FILING DATE: 08-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0695
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-111-470-4

Query Match 19.8%; Score 253; DB 3; Length 316;
Best Local Similarity 29.2%; Pred. No. 2.8e-20;
Matches 78; Conservative 27; Mismatches 86; Indels 76; Gaps 11;

QY 10 VRKNEKSSGIN-----ASSASKERT-APLKSNT-GFPKLLCASLIFLLLAIS 60
DB 70 VLRTRDSNFTSNVAEIALTSOGSSLEETIASLKAVEGFKORQAGV----- 119

QY 61 FFIAFVIFQYKSLLEKTKELVHTTECVKKNMPVEE----- 99
DB 120 -----SEQETTTOKAHLGHCPSPVCVPHSMMLLRVQQLVQDLKLTCTQV 167

QY 100 -----ETAWSCCPKMKSFSSNCYFISTESASMODEKDCARMAHLVINTQEDQF 152

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Db 168 ATINNASTEGTCCPVNWEHODSCYWFSGMSMAEAERYCOLKNAHLVINSREQNP 227
QY 153 IFQNLQESAY-FVGLSDPEGORHQMVDOTPYNESSTFWHHPREPSD-----PNERCV 204
Db 228 VOKYL--GSAITWMLSDPEGA--WKWVDGTDTATGQNNKPCQPDPMOCHGLGGEDCA 283
QY 205 VLNFRKSPKRMGNNDVNCJLGPORSVCE 231
Db 284 --HFHPDGR--WDDVCORPYHWCE 305
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Search completed: August 4, 2003, 13:12:15
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 13:10:58 ; Search time 52 Seconds

(without alignments)
541.270 Million cell updates/sec

Title: US-09-862-802-2

Perfect score: 1280
Sequence: 1 MISEITFAEVRKNEKSSG.....NDVNCIGPQSRVCEMKIHL 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppa/PC7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	10	US-09-862-802-2
2	1273	99.5	237	10	US-09-870-759-49
3	1267	99.0	243	9	US-09-764-870-464
4	1267	99.0	243	15	US-10-125-540-464
5	1267	99.0	246	9	US-09-764-870-303
6	1267	99.0	246	15	US-10-125-540-303
7	612.5	52.5	238	10	US-09-862-802-8
8	552	43.1	211	15	US-10-220-946-22
9	551.5	43.1	213	14	US-10-090-466-2
10	551.5	43.1	213	15	US-10-220-946-20
11	534.5	41.8	182	14	US-10-090-466-4
12	330	25.8	219	10	US-09-809-320-377
13	330	25.8	219	10	US-09-909-0888-377
14	330	25.8	219	10	US-09-905-291A-377
15	330	25.8	219	10	US-09-965-529-3

16	330	25.8	219	10	US-09-902-853-377	Sequence 377, App
17	330	25.8	219	10	US-09-907-824-377	Sequence 377, App
18	330	25.8	219	10	US-09-907-841-377	Sequence 377, App
19	330	25.8	219	11	US-09-904-011-377	Sequence 377, App
20	330	25.8	219	11	US-09-906-742-377	Sequence 377, App
21	330	25.8	219	11	US-09-906-838-377	Sequence 377, App
22	330	25.8	219	11	US-09-907-613-377	Sequence 377, App
23	330	25.8	219	11	US-09-907-942-377	Sequence 377, App
24	330	25.8	219	11	US-09-904-859-377	Sequence 377, App
25	330	25.8	219	11	US-09-909-204-377	Sequence 377, App
26	330	25.8	219	11	US-09-904-820-377	Sequence 377, App
27	330	25.8	219	11	US-09-904-786-377	Sequence 377, App
28	330	25.8	219	11	US-09-906-646-377	Sequence 377, App
29	330	25.8	219	11	US-09-906-700-377	Sequence 377, App
30	330	25.8	219	11	US-09-903-786-377	Sequence 377, App
31	330	25.8	219	11	US-09-902-903-377	Sequence 377, App
32	330	25.8	219	11	US-09-903-749A-377	Sequence 377, App
33	330	25.8	219	11	US-09-904-119-377	Sequence 377, App
34	330	25.8	219	11	US-09-904-956-377	Sequence 377, App
35	330	25.8	219	11	US-09-902-736-377	Sequence 377, App
36	330	25.8	219	11	US-09-907-794-377	Sequence 377, App
37	330	25.8	219	11	US-09-903-943-377	Sequence 377, App
38	330	25.8	219	11	US-09-904-462-377	Sequence 377, App
39	330	25.8	219	11	US-09-907-925-377	Sequence 377, App
40	330	25.8	219	11	US-09-902-692-377	Sequence 377, App
41	330	25.8	219	11	US-09-903-520-377	Sequence 377, App
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43	330	25.8	219	11	US-09-909-064-377	Sequence 377, App
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45	330	25.8	219	11	US-09-905-381-377	Sequence 377, App

ALIGNMENTS

RESULT 1
US-09-862-802-2
; Sequence 2, Application US/09862802
; Patent No. US20020165346A1
; GENERAL INFORMATION:
; APPLICANT: Schering-Plough Corporation
; TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
; FILE REFERENCE: SF0695B
; CURRENT APPLICATION NUMBER: US/09/862,802
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/111,470
; PRIOR FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: mammalian protein
US-09-862-802-2

Query Match 100.0%; Score 1280; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 9, 7e-122;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTSRITFAEVRKNEKSSGINASSAASERTAPLKSNGFPKLLCASLIFLLAIS 60
Db 1 MTSRITFAEVRKNEKSSGINASSAASERTAPLKSNGFPKLLCASLIFLLAIS 60
QY 61 FFIAFVFFQKYSQLEKTKTKLVHTTLCVKNMPEETAWSCCPKNNKSSSNCYFI 120
Db 61 FFIAFVFFQKYSQLEKTKTKLVHTTLCVKNMPEETAWSCCPKNNKSSSNCYFI 120
QY 121 STSASWDSKDCARAEHLVINTOEODFTIUNLOESATYVGLSDPEGARHWQVD 180
Db 121 STSASWDSKDCARAEHLVINTOEODFTIUNLOESATYVGLSDPEGARHWQVD 180

OY 181 QPYNESSTFWHPRPSDPNRCVYLNFRKSPKRWGMDVNCIGPORSVCMMKIHL 237
Db 181 QPYNESSTFWHPRPSDPNRCVYLNFRKSPKRWGMDVNCIGPORSVCMMKIHL 237

RESULT 2

US-09-870-759-49
; Sequence 49, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentln version 3.1
EQ ID NO 49
LENGTH: 237
TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-49

Query Match 99.5%; Score 1273; DB 10; Length 237;
Best Local Similarity 99.6%; Pred. No. 5e-121;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MTSETTYAEVRKNEFKSSGINTASSAASKERTAPLKSNTGPPKLLCASLIFFLLAISF 60
Db 1 MTSETTYAEVRKNEFKSSGINTASSAASKERTAPLKSNTGPPKLLCASLIFFLLAISF 60
OY 61 FFIATVIFFOKYSOLLEKTTKELVHTTLECYKKNMPEETAMSCCPKRWKSFSSNCYFI 120
Db 61 FFIATVIFFOKYSOLLEKTTKELVHTTLECYKKNMPEETAMSCCPKRWKSFSSNCYFI 120
OY 121 STESASWDSKDCARMEAHLLVINTQEOEDFIFONLQESAYFVGLSDPEGQRHWQVD 180
Db 121 STESASWDSKDCARMEAHLLVINTQEOEDFIFONLQESAYFVGLSDPEGQRHWQVD 180
OY 181 QPYNESSTFWHPRPSDPNRCVYLNFRKSPKRWGMDVNCIGPORSVCMMKIHL 237
Db 181 QPYNESSTFWHPRPSDPNRCVYLNFRKSPKRWGMDVNCIGPORSVCMMKIHL 237

RESULT 3

US-09-764-870-464
; Sequence 464, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 464
LENGTH: 243
TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-464

Query Match 99.0%; Score 1267; DB 9; Length 243;
Best Local Similarity 99.6%; Pred. No. 2.1e-120;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEITTAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGPPKLLCASLIFFLLAISF 62
Db 9 SEITTAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGPPKLLCASLIFFLLAISF 68

OY 63 IAFVIFFOKYSOLLEKTTKELVHTTLECYKKNMPEETAMSCCPKRWKSFSSNCYFI 122
Db 63 IAFVIFFOKYSOLLEKTTKELVHTTLECYKKNMPEETAMSCCPKRWKSFSSNCYFI 128
OY 123 ESASWDSKDCARMEAHLLVINTQEOEDFIFONLQESAYFVGLSDPEGQRHWQVD 182
Db 123 ESASWDSKDCARMEAHLLVINTQEOEDFIFONLQESAYFVGLSDPEGQRHWQVD 188
OY 183 PYNESSTFWHPRPSDPNRCVYLNFRKSPKRWGMDVNCIGPORSVCMMKIHL 237
Db 183 PYNESSTFWHPRPSDPNRCVYLNFRKSPKRWGMDVNCIGPORSVCMMKIHL 243

RESULT 4

US-10-125-540-464
; Sequence 464, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 464
LENGTH: 243
TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-464

Query Match 99.0%; Score 1267; DB 15; Length 243;
Best Local Similarity 99.6%; Pred. No. 1e-120;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEITTAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGPPKLLCASLIFFLLAISF 62
Db 9 SEITTAEVFRKNEFKSSGINTASSAASKERTAPLKSNTGPPKLLCASLIFFLLAISF 68
OY 63 IAFVIFFOKYSOLLEKTTKELVHTTLECYKKNMPEETAMSCCPKRWKSFSSNCYFI 122
Db 63 IAFVIFFOKYSOLLEKTTKELVHTTLECYKKNMPEETAMSCCPKRWKSFSSNCYFI 128
OY 123 ESASWDSKDCARMEAHLLVINTQEOEDFIFONLQESAYFVGLSDPEGQRHWQVD 182
Db 123 ESASWDSKDCARMEAHLLVINTQEOEDFIFONLQESAYFVGLSDPEGQRHWQVD 188
OY 183 PYNESSTFWHPRPSDPNRCVYLNFRKSPKRWGMDVNCIGPORSVCMMKIHL 237
Db 183 PYNESSTFWHPRPSDPNRCVYLNFRKSPKRWGMDVNCIGPORSVCMMKIHL 243

RESULT 5

US-09-764-870-303
; Sequence 303, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 303
LENGTH: 246
TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-303

Query Match 99.0%; Score 1267; DB 9; Length 246;

Best Local Similarity 99.6%; Pred. No. 2,1e-120;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SETTYAEVRKRNKFNKSGINTASSASKERTAPLAKSNTGPKLLCASLIFLLLAISFF 62
Db 12 AETTYAEVRKRNKFNKSGINTASSASKERTAPLAKSNTGPKLLCASLIFLLLAISFF 71
QY 63 IAFVIFFOKYSQLEKKTTELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 122
Db 72 IAFVIFFOKYSQLEKKTTELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 131
QY 123 ESASWODEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORHMOVDOT 182
Db 132 ESASWODEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORHMOVDOT 191
QY 183 PYNESSTFWHPRPSDPNERCIVLNFRRKSPKRMGMNDVNLGQORSVCENMKIHL 237
Db 192 PYNESSTFWHPRPSDPNERCIVLNFRRKSPKRMGMNDVNLGQORSVCENMKIHL 246

RESULT 6

Sequence 303, Application US/10125540
Publication No. US20030059875A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 303
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-540-303

Query Match 99.0%; Score 1267; DB 15; Length 246;
Best Local Similarity 99.6%; Pred. No. 2,1e-120;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SETTYAEVRKRNKFNKSGINTASSASKERTAPLAKSNTGPKLLCASLIFLLLAISFF 62
Db 12 AETTYAEVRKRNKFNKSGINTASSASKERTAPLAKSNTGPKLLCASLIFLLLAISFF 71
QY 63 IAFVIFFOKYSQLEKKTTELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 122
Db 72 IAFVIFFOKYSQLEKKTTELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 131
QY 123 ESASWODEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORHMOVDOT 182
Db 132 ESASWODEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORHMOVDOT 191
QY 183 PYNESSTFWHPRPSDPNERCIVLNFRRKSPKRMGMNDVNLGQORSVCENMKIHL 237
Db 192 PYNESSTFWHPRPSDPNERCIVLNFRRKSPKRMGMNDVNLGQORSVCENMKIHL 246

RESULT 7

US-09-862-802-8
Sequence 8, Application US/09862802
Patent No. US20020165346A1

GENERAL INFORMATION:
APPLICANT: Schering-Plough Corporation
TITLE OF INVENTION: MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
FILE REFERENCE: SF0695B
CURRENT APPLICATION NUMBER: US/09/862,802
CURRENT FILING DATE: 2002-01-10
Prior Application Number: US 09/111,470
Prior Filing Date: 1998-07-08
NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patent In version 3.1

SEQ ID NO 8
LENGTH: 238
TYPE: PRT
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: mammalian protein
US-09-862-802-8

Query Match 52.5%; Score 672.5; DB 10; Length 238;
Best Local Similarity 53.3%; Pred. No. 3,7e-60;
Matches 129; Conservative 37; Mismatches 67; Indels 9; Gaps 6;

QY 1 MTSEITYAEVRKRNKFNKSGINTASSASKERTAPLAKS--NTGPKLLCASLIFLLLA 58
Db 1 MASEITYAEVRKRNKFNKSGINTASSASKERTAPLAKS--NTGPKLLCASLIFLLLA 58
QY 59 ISEFFIAFVIFFOKYSQLEKKTTELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 117
Db 59 ISEFFIAFVIFFOKYSQLEKKTTELVTLECYKKNMPVEETAMSCCPKMKSFSSNCFIST 118
QY 118 YFIST--ESASWODEKDCARMEAHLLVINTQEOEDFIFONLOESAYFVGLSDPEGORH 175
Db 119 YLVPVSSASAMKSEKNCRMGAHLVIOEOEDFIFONLOESAYFVGLSDPEGORH 177
QY 176 WQWVDOTPYNESSTFWHPRPSDPNERCIVLNFRRKSPKRMGMNDVNLGQORSVCENMKI 235
Db 178 WQWVDOTPYNESSTFWHPRPSDPNERCIVLNFRRKSPKRMGMNDVNLGQORSVCENMKI 236
QY 236 HL 237
Db 237 NL 238

RESULT 8

US-10-220-946-22
Sequence 22, Application US/10220946
Publication No. US20030124575A1

GENERAL INFORMATION:
APPLICANT: NO. US20030124575A1artis AG
APPLICANT: No. US20030124575A1artis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: Werner, William
APPLICANT: Jentz, Gudrun
APPLICANT: Lapp, Hilmar
APPLICANT: Kalthoff, Frank Stephan
TITLE OF INVENTION: Organic Compounds
FILE REFERENCE: 4-31347 PCT
CURRENT APPLICATION NUMBER: US/10/220,946
CURRENT FILING DATE: 2002-09-06
Prior Application Number: US 60/192,934
Prior Filing Date: 2000-03-29
Prior Application Number: US 60/205,026 (US 60/279,243)
Prior Filing Date: 2000-05-18
Prior Application Number: US 60/205,020
Prior Filing Date: 2000-05-18
Prior Application Number: US 60/205,769
Prior Filing Date: 2000-05-19
Prior Application Number: US 60/205,767
Prior Filing Date: 2000-05-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 211
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-220-946-22

Query Match 43.1%; Score 552; DB 15; Length 211;
Best Local Similarity 47.7%; Pred. No. 5,2e-48;
Matches 102; Conservative 42; Mismatches 60; Indels 10; Gaps 4;

QY 28 ASKERTAPLAKSNTGPKLLCASLIFLLLAISFFIAFVIF--FOKYSQLEKKTTELVTLE 83

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Db 4 ASEDDE---KGLMWOLKYMNAVYVILLSCFVSSVPHNFMYSKTKRLSKIREQ 60
QY 84 LVHTLECYKKNMPEETAMSCCPKNWKSFSNSNCYFISTESAMODSEDCARMEAHILY 143
Db 61 QYHPSLTCVMEKDIED--WSCCPYMTSFOSSCYFISTGMSQKNCVGMGADLV 118
QY 144 INTOEODIFONLOESAYFVGLSDPEGRHQMWDQTPYNESSTFMHREPSDNERC 203
Db 119 INTREODPFIIONLKRNSYFGLSDPGRHQMWDQTPYENVTFMHSGEPNLDERC 178
QY 204 VTLNFRKSPKMGMDVNCGLGPRSCVCEMKIHL 237
Db 179 ALINFRSS-EEMGWMDIHCHVPOKSKICKKIYI 211

RESULT 9
US-10-090-466-2
Sequence 2, Application US/10090466
Publication No. US20020137914A1
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
TITLE OF INVENTION: NO. US20020137914A1 Human Declin Proteins and Polynucleotides
FILE REFERENCE: LEX-0315-USA
CURRENT APPLICATION NUMBER: US/10/090,466
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/274,961
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 213
TYPE: PRT
ORGANISM: homo sapiens
US-10-090-466-2

Query Match 43.1%; Score 551.5; DB 14; Length 213;
Best Local Similarity 50.8%; Pred. No. 6e-48;
Matches 97; Conservative 38; Mismatches 49; Indels 7; Gaps 3;

QY 51 LIFLLAISFIATVI---FQKYSQLLEKTKTELVTHTLECYKKNMPEETAMSCC 106
Db 26 VVSIILLSCYFVSSVPHNFMYSKTKRLSKIREQOYHPSLTCVMEKDIED--WSCC 83
QY 107 PKNWKSFSNSNCYFISTESAMODSEDCARMEAHILVINTREODPFIIONLOESAYFVG 166
Db 84 PTPWTSFOSSCYFISTGMSQKNCVGMGADLVINTREODPFIIONLKRNSYFLG 143
QY 167 LSDPGRHQMWDQTPYNESSTFMHREPSDNERCVTLNFRKSPKMGMDVNCGLGPO 226
Db 144 LSDPGRHQMWDQTPYENVTFMHSGEPNLDERCALINFRSS-EEMGWMDIHCHVPO 202
QY 227 RSVCEMKIHL 237
Db 203 KSKICKKIYI 213

RESULT 10
US-10-220-946-20
Sequence 20, Application US/10220946
Publication No. US20030124575A1
GENERAL INFORMATION:
APPLICANT: No. US20030124575A1artis AG
APPLICANT: No. US20030124575A1artis Erfindungen Verwaltungsgesellschaft m.B.H.
APPLICANT: Phares, William
APPLICANT: Werner, Gudrun
APPLICANT: Jaritz, Markus
APPLICANT: Lapp, Hilmar
APPLICANT: Kalchoff, Frank Stephan
TITLE OF INVENTION: Organic Compounds
FILE REFERENCE: 4-31347 PCT
```

```
QY 51 LIFLLAISFIATVI---FQKYSQLLEKTKTELVTHTLECYKKNMPEETAMSCC 106
Db 31 VVSIILLSCYFVSSVPHNFMYSKTKRLSKIREQOYHPSLTCVMEKDIED--WSCC 88
QY 107 PKNWKSFSNSNCYFISTESAMODSEDCARMEAHILVINTREODPFIIONLOESAYFVG 166
Db 89 PTPWTSFOSSCYFISTGMSQKNCVGMGADLVINTREODPFIIONLKRNSYFLG 148
QY 167 LSDPGRHQMWDQTPYNESSTFMHREPSDNERCVTLNFRKSPKMGMDVNCGLGPO 226
Db 149 LSDPGRHQMWDQTPYENVTFMHSGEPNLDERCALINFRSS-EEMGWMDIHCHVPO 207
QY 227 RSVCEMKIHL 237
Db 208 KSKICKKIYI 218

RESULT 11
US-10-090-466-4
Sequence 4, Application US/10090466
Publication No. US20020137914A1
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
TITLE OF INVENTION: NO. US20020137914A1 Human Declin Proteins and Polynucleotide
FILE REFERENCE: LEX-0315-USA
CURRENT APPLICATION NUMBER: US/10/090,466
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/274,961
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 182
TYPE: PRT
ORGANISM: homo sapiens
NAME/KEY: VARIANT
LOCATION: (1)...(182)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-090-466-4

Query Match 41.8%; Score 534.5; DB 14; Length 182;
Best Local Similarity 54.4%; Pred. No. 2.6e-46;
Matches 92; Conservative 31; Mismatches 43; Indels 3; Gaps 2;

QY 69 FQKYSQLLEKTKTELVTHTLECYKKNMPEETAMSCCPKNWKSFSNSNCYFISTESASQ 128
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Db 17 YSKTVKRLSKIREQYHXSLTCVMECKDIED--WSCCPRTWTSFOSSCYFISTGMSWT 74
QY 129 DSEKCARMEAHLLVINTOEODFIPTONLOESAYFVGLSDPESQRHMWDOTPYESS 188
Db 75 KSOQNCVSMGADLVINTREODFIPTONLKRNSYFGLSDPGGRHMWDOTPYENY 134
QY 189 TFWHPRPSDPNRCVVLNFRKSPKRWGMNDVNCIGPQRSVCMMKITHL 237
Db 135 TFWHSGEPNNLDERCAITINFRSS-EEWGMNDHCHVQKSIKMKKIYI 182

RESULT 12
US-09-909-320-377
; Sequence 377, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 377
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-377

Query Match 25.8%; Score 330; DB 10; Length 219;
Best Local Similarity 38.0%; Pred. No. 1.8e-25;
Matches 70; Conservative 29; Mismatches 79; Indels 6; Gaps 3;

QY 55 LLTAISFFIAVFIFQKYSOLLEKTKKELVHTLECVKKNMPEETAWSCCPKMKFS 114
Db 32 LFLSACFTTRCVYFRFQCODEKKFOLPENFTFLSCYNG---SGSVKNCCPLNMEYFQ 88
QY 115 SNCYFISTESASWODEKDCARMEAHLLVINTOEODFIPTONLOESAYFVGLSDPGQR 174
Db 89 SSCYFFSTDTISWALSILKNCSSAMGADLVINSOEQEFLLSYKKPKMREFFIGLSDQYVEG 148
QY 175 HMCWVDOTPYNESTFWHPRPSD--PNERCVVLNFRKSPKRWGMNDVNCIGPQRSVCEM 232
Db 149 QMCWVDGTPLEKSLSFWDVGPNNIATLEDCATIRDSNP-RQNMNDVTCGLNFRICEM 207
QY 233 MKIH 236
Db 208 VGIN 211

RESULT 13
US-09-909-088B-377
; Sequence 377, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

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OM protein - protein search, using sw model

Run on: August 4, 2003, 13:05:58 ; Search time 40 Seconds
(without alignments)
569,799 Million cell updates/sec

Title: US-09-862-802-2

Perfect score: 1280
Sequence: 1 MTSEITYAEVRFKNEKSSG.....NDVNCIGPQSVCEMKIHL 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1280	100.0	237	2 JC7608	type II lectin-like
2	251	19.6	301	2 S13165	asialoglycoprotein
3	235	18.4	301	1 LNRT2	hepatic lectin 2 -
4	228.5	17.9	284	1 LNRTL	hepatic lectin 2 -
5	227.5	17.8	306	2 A42230	lectin M-ASGP-BP P
6	224	17.5	207	1 LNCHL	hepatic lectin - C
7	223.5	17.5	311	1 LNHU2A	asialoglycoprotein
8	221	17.3	284	2 S29855	asialoglycoprotein
9	220.5	17.2	291	1 LNHO1	hepatic lectin HI
10	219.5	17.1	742	2 JC7595	scavenger receptor
11	216.5	16.9	304	2 JX0209	lectin, galactose/
12	208.5	16.3	331	1 LNMSER	IgE Fc receptor, 1
13	207	16.2	1479	2 T42710	IgE Fc receptor, 1
14	205.5	16.1	309	1 S34198	mannose receptor, II
15	205.5	16.1	404	2 A46274	HIV gp120-binding
16	196	15.3	550	2 A28166	Kupffer cell recep
17	187	14.6	1268	2 S52781	neurocan - mouse
18	184	14.4	1257	2 S28764	neurocan precursor
19	183.5	14.3	2124	2 A28452	proteoglycan core
20	181	14.1	1340	2 A39808	proteoglycan core
21	181	14.1	2327	2 T42630	aggreacan - bovine
22	176	13.8	2109	1 T50421	aggreacan precursor
23	176	13.8	2132	1 A55182	aggreacan precursor
24	176	13.8	2415	1 A39086	NKR-p1 protein hom
25	175.5	13.7	220	2 C46467	reg II, regenerati
26	174	13.6	173	2 B47148	mannose receptor p
27	172.5	13.5	1455	1 A48925	mannose receptor p
28	171.5	13.4	1456	1 A36563	mannose receptor p
29	171	13.4	266	2 I49059	Ly49c - mouse

30	170.5	13.3	155	2 S78774	perlecan - Halioti
31	170	13.3	223	2 B46467	NKR-p1 protein hom
32	169	13.2	257	2 I50146	gene 17.5 protein
33	168	13.1	883	2 S57653	brevican precursor
34	168	13.1	3562	2 A47171	chondroitin sulfate
35	167	13.0	153	1 A43413	antifreeze protein
36	167	13.0	173	2 S10548	lectin - barnacle
37	167	13.0	216	2 PT0375	natural killer cel
38	167	13.0	912	2 A54423	brevican precursor
39	166	13.0	330	2 T46256	brevican human (
40	165.5	12.9	321	1 LNHOER	IgE Fc receptor II
41	165	12.9	883	2 S49126	brevican precursor
42	164	12.8	223	2 A35917	NK-cell receptor p
43	162.5	12.7	227	2 A46467	natural killer cel
44	159.5	12.5	162	1 LNRC3	lectin-BRA3-2 prec
45	157	12.3	266	2 I49363	natural killer cel

ALIGNMENTS

RESULT 1

JC7608 type II lectin-like immunoreceptor - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C:Accession: JC7608

R: Huang, X.; Yuan, Z.; Chen, G.; Zhang, M.; Zhang, W.; Yu, Y.; Cao, X.

Biochem. Biophys. Res. Commun. 281, 131-140, 2001

A:Title: Cloning and characterization of a novel ITIM containing lectin-like immunore

A:Reference number: JC7608; PMID:21092797; PMID:11178971

A:Contents: Dendritic cells

A:Accession: JC7608

A:Molecule type: mRNA

A:Residues: 1237 <HDA>

A:Comments: References: GB:AF067800

C:Comment: This receptor, highly homologous to the group of macrophage/hepatic lectin

cell, especially in migrating, antigen capturing and processing.

C:Genetics:

A:Gene: 111r

A:Map position: 12p13

F:45-69/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 1280; DB 2; Length 237;
Best Local Similarity 100.0%; Pred No. 14e-105;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTSEITYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGPKLLCASLIFLLAIS 60		1	MTSEITYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGPKLLCASLIFLLAIS 60
DB	1	MTSEITYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGPKLLCASLIFLLAIS 60		1	MTSEITYAEVRFKNEKSSGINTASSAASKERTAPLKSNTGPKLLCASLIFLLAIS 60
QY	61	FFIAFYIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETANSCCPKMKSSSCYFI 120		61	FFIAFYIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETANSCCPKMKSSSCYFI 120
DB	61	FFIAFYIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETANSCCPKMKSSSCYFI 120		61	FFIAFYIFFOKYSQLEKTKTKELVHTTLECVKKNMPVEETANSCCPKMKSSSCYFI 120
QY	121	STFSASMODESKCARMEALVINTQEBDFIFONLOESAFVGLSDPEGRHQMWD 180		121	STFSASMODESKCARMEALVINTQEBDFIFONLOESAFVGLSDPEGRHQMWD 180
DB	121	STFSASMODESKCARMEALVINTQEBDFIFONLOESAFVGLSDPEGRHQMWD 180		121	STFSASMODESKCARMEALVINTQEBDFIFONLOESAFVGLSDPEGRHQMWD 180
QY	181	QTPYNESSTFWHDREPSDPERNCVNLNFRKSPRKMGMNDVNCIGPQSVCEMKIHL 237		181	QTPYNESSTFWHDREPSDPERNCVNLNFRKSPRKMGMNDVNCIGPQSVCEMKIHL 237
DB	181	QTPYNESSTFWHDREPSDPERNCVNLNFRKSPRKMGMNDVNCIGPQSVCEMKIHL 237		181	QTPYNESSTFWHDREPSDPERNCVNLNFRKSPRKMGMNDVNCIGPQSVCEMKIHL 237
RESULT 2					
S13165		asialoglycoprotein receptor - mouse			
N:Alternate names:		hepatic lectin			
C:Species:		Mus musculus (house mouse)			
C:Date:		21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999			
C:Accession:		S13165			
R:Sanford, J.P.; Doyle, D.		Biochim. Biophys. Acta 1087, 259-261, 1990			

A>Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor genes
 A:Reference number: S13165; MUID:91027942; PMID:2223888
 A:Accession: S13165
 A:Molecule type: mRNA
 A:Residues: 1-301 <SAND>
 A:Cross-references: EMBL:X53042; NID:953104; PIDN:CAA37211.1; PID:953105
 C:Superfamily: hepatic lectin; C-type lectin homology
 C:Keywords: glycoprotein; liver; transmembrane protein
 F:170-293/Domain: C-type lectin homology <LCH>

Query Match 19.6%; Score 251; DB 2; Length 301;
 Best Local Similarity 25.2%; Pred. No. 1.2e-14;
 Matches 65; Conservative 38; Mismatches 75; Indels 80; Gaps 7;

42 FPKLLCASLLIFLLAISFFIAFYI-----FFQKVS----- 73
 49 FPKRLCSFRLSLALANILLVIVCVSSOSIOLOEERFLKELTFSSSTLMERGA 108
 74 -----OLLEKKTKEIVHTTECVKKNMPV-----ETAWMS 104
 109 LDTLGSTNAILTSMWADLEEKQOLKADHSTLFLHLPMDLRTILCOLAYFQSGTE 168
 QY 105 CCPKMKSFSSNCYFISTESASMODSEKDCARMEAHLLVINTOEODFFQNLQESAVF 164
 DB 169 CCPVNWVEFGSGCTWFSDGLTVAEDQYCOLENAHLVINTSREKQDPVVKH-RSOFHIW 227
 QY 165 VGLSDPEGORHMQWVDQTPYNESSYFWHPRESDPNERCVLVNFKRSPKRMG----- 216
 DB 228 IGLTDRDGS--WKWVDGTEYRSNFRNMAFTQDP-----NMGGHGGGSGEDCAELIIS 276
 QY 217 ---WADVNCLEPQRSVCE 231
 DB 277 DGHWNDFNCQOVNRYWVCE 294

RESULT 3

LNRT2
 hepatic lectin 2 - rat

N:Alternate names: asialoglycoprotein receptor RHL-2/3 (ASGP-R2/3)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1988 #sequence,revision 09-Apr-1998 #text,change 22-Jun-1999

C:Accession: B28462; A28462; A31601; A26888; A25417
 R:Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, J.
 J. Biol. Chem. 262: 9628-9636, 1987
 A>Title: Major and minor forms of the rat liver asialoglycoprotein receptor are independent
 A:Reference number: A28462; MUID:87250565; PMID:3597443
 A:Accession: B28462
 A:Molecule type: mRNA
 A:Residues: 1-301 <HAL>
 A:Cross-references: GB:J02762; NID:9205162; PIDN:AAA41522.1; PID:9205163
 A:Accession: A28462

A:Molecule type: protein
 A:Residues: 88-96, 'X', 98-118, 'X', 120-129-158-177-182, 'X', 184, 'X', 186-189, 192-290, 'C', 292
 R:Sanford, J.P.; Elliott, R.W.; Doyle, D.
 DNA 7, 721-728, 1988

A>Title: Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.
 A:Reference number: A31601; MUID:89170119; PMID:3234178
 A:Accession: A31601

A:Molecule type: mRNA
 A:Residues: 1-301 <SAND>
 A:Cross-references: GB:X07636; NID:957066; PIDN:CAA30476.1; PID:957067
 R:McPhaul, M.; Berg, P.
 Mol. Cell. Biol. 7, 1841-1847, 1987
 A>Title: Identification and characterization of cDNA clones encoding two homologous prot
 A:Reference number: A26888; MUID:87257885; PMID:3600647
 A:Accession: A26888

A:Molecule type: mRNA
 A:Residues: 1-152, 'A', 154-201, 'T', 203-259, 'C', 261-301 <MCP>
 A:Cross-references: GB:M16347; NID:9206648; PIDN:AAA42038.1; PID:9206649
 A>Note: the authors translated the codon GCA for residue 153 as Arg and ATT for residue
 R:Drickamer, K.; Memon, J.F.; Blinn, G.; Leung, J.O.
 J. Biol. Chem. 259, 770-778, 1984

A>Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evid

A:Reference number: A25417; MUID:84111554; PMID:6319386
 A:Accession: A25417
 A:Molecule type: protein
 A:Residues: 201-259, 'C', 261-281, 'ND', 284-301 <DR1>
 C:Comment: Calcium is required for ligand binding.
 C:Superfamily: hepatic lectin; C-type lectin homology
 C:Keywords: endocytosis; glycoprotein; lectin; liver; receptor; transmembrane protein
 F:2-60/Domain: intracellular #status predicted <INT>
 F:61-77/Domain: transmembrane #status predicted <TRN>
 F:78-301/Domain: extracellular #status predicted <EXT>
 F:170-293/Domain: C-type lectin homology <LCH>
 F:97,119,165/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 18.4%; Score 235; DB 1; Length 301;
 Best Local Similarity 25.6%; Pred. No. 3.1e-13;
 Matches 66; Conservative 39; Mismatches 73; Indels 80; Gaps 11;

42 FPKLLCASLLIFLLAISFFIAFYI-----FQK----- 71
 49 FPKRLCSFRLSLALANILLVIVCVSSOSMOLOEFWTLKELTSLNFTTLMERKA 108
 72 -----YSOLLEKKTKEIV--HTTECVKKNMPVE-----ETAW 103
 QY 109 LSHGGSNDNLTSMETLEKK-QDKADHSTLFLHLPMDLRTILCOLAYFLSNGT 167
 DB 104 SCCPKMKSFSSNCYFISTESASMODSEKDCARMEAHLLVINTOEODFFQNLQESAV 163
 QY 168 ECCPVNWVEFGSGCTWFSDGLTVAEDQYCOMENAHLLVINTSREGEFV--YKHGAF 224
 DB 164 --FVGLSDPEGORHMQWVDQTPYNESSYFWHPRESD-----PNEGCV-VLNRKSPK 213
 QY 225 HIWIGLTDKDS--WKWVDGTEYRSNFRNMAFTQDPNMGGHEGSGEDCAELISGL--- 279
 DB 214 RMGNDVNCLEPQRSVCE 231
 DB 280 ---WNDNFCQOVNRYWVCE 294

RESULT 4

LNRT1
 hepatic lectin - rat

N:Alternate names: ASGP; asialoglycoprotein receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Feb-1986 #sequence,revision 04-Dec-1986 #text,change 22-Jun-1999

C:Accession: A92497; A94020; B94020; A54727; A03166
 C:Accession: A92497; A94020; B94020; A54727; A03166
 R:Leung, J.O.; Holland, E.C.; Drickamer, K.
 J. Biol. Chem. 260, 12523-12527, 1985

A>Title: Characterization of the gene encoding the major rat liver asialoglycoprotein
 A:Reference number: A92497; MUID:86008355; PMID:2995379
 A:Accession: A92497

A:Molecule type: DNA
 A:Residues: 1-284 <LEB>
 A:Cross-references: GB:K02817; NID:9206646; PIDN:AAA42037.1; PID:9206647
 R:Holland, E.C.; Leung, J.O.; Drickamer, K.

Proc. Natl. Acad. Sci. U.S.A. 81, 7338-7342, 1984

A>Title: Rat liver asialoglycoprotein receptor lacks a cleavable NH-2-terminal signal
 A:Reference number: A94020; MUID:85063786; PMID:6095287
 A:Accession: A94020

A:Molecule type: mRNA
 A:Residues: 1-60, 'R', 62-210 <HO1>
 A:Experimental source: clone 22; clone 1
 A:Accession: B94020
 A:Molecule type: mRNA
 A:Residues: 92-284 <HO2>
 A>Note: clone 22 codes for a terminator at residue 210
 R:Watts, C.

Biosci. Rep. 6, 527-534, 1986

A>Title: Isolation and expression of cDNA clones for a rat liver asialoglycoprotein r
 A:Reference number: A54727; MUID:87026895; PMID:2945599
 A:Accession: A54727

A:Molecule type: mRNA
 A:Residues: 12-284 <NAT>

A:Cross-references: GB:M21770; NID:9202985; PIDN:AAA40764.1; PID:9202988

A:Experimental source: liver
 C:Comment: Two types of rat hepatic lectin have been identified, RHL-1 and RHL-2/3, having
 C:Comment: After removal of sialic acid monomers from the complex carbohydrate moieties
 C:Comment: The unusual orientation of this protein across the membrane is postulated to
 C:Genetics:

A:Introns: 23/1; 62/1; 118/1; 147/1; 197/3; 233/2
 C:Species: hepatic lectin; C-type lectin homology
 C:Superfamily: glycoprotein; lectin; receptor; transmembrane protein
 C:Keywords: endocytosis; glycoprotein; lectin; receptor; transmembrane protein
 F:2-284/Product: hepatic lectin #status predicted <INT>
 F:2-39/Domain: intracellular #status predicted <INT>
 F:40-60/Domain: transmembrane #status predicted <INT>
 F:61-284/Domain: extracellular #status predicted <EXT>
 F:153-276/Domain: C-type lectin homology <LCH>
 F:75,78,146/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 17.9%; Score 228.5; DB 1; Length 284;
 Best Local Similarity 23.6%; Pred. No. 1.1e-12;
 Matches 61; Conservative 36; Mismatches 84; Indels 77; Gaps 8;

43 PKL---LCASLIFELLATSFIAFYF-----FQKYSQLEKTKTRELVT-----TLECVKKNMPVEE 100
 28 PRLQRLCSGFRLLLSIGLSILLVVCVITSONSQRLEDRVLRQNFNFYSTEDEV 87
 69 -----FQKYSQLEKTKTRELVT-----TLECVKKNMPVEE 100

88 KALTQGERVGRKKMKLVESQLEKHQEDLRHDSRLHLVKQLVSDVRSLSQOMALRGNG 147
 101 TAWSCCCKRNKSFSSNCFYFSTESASWQSDSEKDCARMAHLVINTQEDQFIONLOE 160
 148 SERICCPINWVEYSGSCWSSSVKVPTEADKCYOLENAHLVYVTSWSEQRFVQOHMGPL 207

161 SAVFVGLSDPEGRHMQWVDQTPYNESSTFWHPREPSD-----PNERCVLNFRRKSPK 213
 208 NTF-IGLELDQNGP--WKWVDCTDYEETGRKNRPGQPDWYGHGLGGEDCA--HFTTDCG 262
 214 RWGNVDNCLGQPSRVC 231
 263 --WDDVCCRPRYRWCE 277

RESULT 5
 A42230
 A:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 20-Aug-1999
 C:Accession: A42230
 R:11; M.; Kurata, H.; Itoh, N.; Yamashina, I.; Kawasaki, T.
 J. Biol. Chem. 265, 11295-11298, 1990
 A:Title: Molecular cloning and sequence analysis of cDNA encoding the macrophage lectin
 A:Reference number: A42230; MUID:90293078; PMID:2358462
 A:Accession: A42230
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-306 <I>
 A:Cross-references: GB:J05495; NID:9204302; PIDN:AAA41216.1; PID:9204303
 C:Superfamily: hepatic lectin; C-type lectin homology
 F:175-298/Domain: C-type lectin homology <LCH>

Query Match 17.8%; Score 227.5; DB 2; Length 306;
 Best Local Similarity 31.6%; Pred. No. 1.4e-12;
 Matches 48; Conservative 27; Mismatches 62; Indels 15; Gaps 5;

88 TLECVKKNMPVEETAWSCCKRNKSFSSNCFYFSTESASWQSDSEKDCARMAHLVINTQ 147
 157 TLTQQLASLNKNGSAVACCPHMHHEBSCYWFSGCKPWEADRYCOLENSNLVYVNSL 216
 148 EEDQFIONLOEESAAYFVGLSDPEGRHMQWVDQTPYNESSTFWHPREPSD-----PN 200
 217 AEQNFLL-QTHMGSVVTVIGLELDQNGP--WRWVDGIDYEETGRKNRPGQPDWYGHGLGG 273

201 ERCVYVLFRRKSPKRWGNVDNCLGQPSRVC 232
 274 EDCA--HFTSDGR--WDDVCCRPRYRWCE 300

RESULT 6
 LNCHL
 C:Species: Gallus gallus (chicken)
 C:Date: 08-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 22-Jun-1999
 C:Accession: A03167; A28194; A40427
 R:Drickamer, K.
 J. Biol. Chem. 256, 5827-5839, 1981
 A:Title: Complete amino acid sequence of a membrane receptor for glycoproteins. Sequ
 A:Reference number: A03167; MUID:81215504; PMID:7240175
 A:Accession: A03167
 A:Molecule type: protein
 A:Residues: 1-207 <DR>
 A>Note: some or all of the cysteines are involved in disulfide bonds
 A>Note: residues 24-48 form an uncharged, hydrophobic region that may interact with o
 J. Biol. Chem. 263, 5468-5473, 1988
 A:Title: Endocytosis of N-acetylglucosamine-containing glycoproteins by rat fibroblas
 A:Reference number: A28194; MUID:88186849; PMID:3281941
 A:Accession: A28194
 A:Molecule type: mRNA
 A:Residues: 1-207 <ME>
 A:Cross-references: GB:J03188; NID:9212246; PIDN:AAA48937.1; PID:9212247
 R:Bezouska, K.; Crichton, G.V.; Rose, J.M.; Taylor, M.E.; Drickamer, K.
 J. Biol. Chem. 266, 11604-11609, 1991
 A:Title: Evolutionary conservation of intron position in a subfamily of genes encodin
 A:Reference number: A40427; MUID:91268022; PMID:2050668
 A:Accession: A40427
 A:Molecule type: DNA
 A:Residues: 1-207 <BE>
 A:Cross-references: GB:M63225; GB:M63226; GB:M63227; GB:M63228; GB:M63229; GB:M63230;
 C:Comment: Hepatic lectin is a membrane receptor protein that recognizes and binds ex
 and endocytosis.

C:Genetics:
 A:Introns: 15/1; 50/1; 75/1; 125/3; 163/2
 C:Superfamily: hepatic lectin; C-type lectin homology
 C:Keywords: acetylated amino end; glycoprotein; lectin; transmembrane protein
 F:1-23/Domain: intracellular #status predicted <INT>
 F:24-47/Domain: transmembrane #status predicted <TRA>
 F:48-207/Domain: extracellular #status predicted <EXT>
 F:78-201/Domain: C-type lectin homology <LCH>
 F:1/Modified site: acetylated amino end (Met) #status experimental
 F:67/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 17.5%; Score 224; DB 1; Length 207;
 Best Local Similarity 27.8%; Pred. No. 1.9e-12;
 Matches 54; Conservative 35; Mismatches 79; Indels 26; Gaps 7;

49 SLILFELLATSFIAFY---IFQKYSQLEKTKTRELVTTLTLECVKKNMPVEETAWSC 105
 24 SFAAVYVLLALSFLLTLTLSSVSLARIALSSKSLTD-----SEPHNNSRSLLEPP 77
 106 C---PKNKSFSNCFYFSTESASWQSDSEKDCARMAHLVINTQEDQFIONLOEESA 162
 78 CGAQRQMEYFEGGRYFYSLSRMSWKKAKACEEHHSLIILDSYAKNPFMERFRNR-R 136

163 YFVGLSDPEGRHMQWVDQTPYNESSTFWHPREPSD--NERCVLNFRRKSPKRW--GW 217
 137 FWIGTIDENQGEWQWVDGTDTRSSFTFWKEGEPNRRGFNBDCAHV-----WTSQGW 188
 218 NDVNCIGQPSRVC 231
 189 NDVYCTTECYVCE 202

RESULT 7
 LNHDZA
 A:Species: Homo sapiens (man)
 C:Superfamily: asialoglycoprotein receptor H2a; asialoglycoprotein receptor H2b
 N:Alternate names: AsGPR; asialoglycoprotein receptor H2a; asialoglycoprotein receptor H2b
 C:Species: Homo sapiens (man)

A:Reference number: JX0209; MUID:92268032; PMID:1587794
A:Accession: JX0209
A:Molecule type: mRNA
A:Residues: 1-304 <SAT>
A:CROSS-references: GB:S5676; NID:g249360; PIDN:AAB22171.1; PID:g249361
R:Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.
J. Biochem. 104, 600-605, 1988
A>Title: Purification and characterization of a lectin-like molecule specific for galactose
A:Reference number: PX0009; MUID:89197865; PMID:3241002
A:Accession: PX0009
A:Molecule type: protein
A:Residues: 102-120;137,'X',139-151 <ODA>
C:Superfamily: hepatic lectin; C-type lectin homology
F:36-61/Domain: transmembrane status predicted <TRA>
E:174-236/Domain: C-type lectin homology <LCH>
F:174,166/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 16.9%; Score 216.5; DB 2; Length 304;
Best Local Similarity 31.1%; Pred. No. 1.3e-11;
Matches 47; Conservative 25; Mismatches 64; Indels 15; Gaps 5;

OY 89 LECYKKNPVETIAMSCCKRWKSFSSNCYITSTESASWQDESDCAMENHLVINTQE 148
.:
DB 156 LTCLDLANKNGSEVACPLMTEHSGCYWFSESSEKSWPADRYCRLENSHLVVNSLE 215
.:
OY 149 EODTIFONLQESAAYFVGLSPDEGORHMOWDOPNYNSSYFMHPREPSD-----PNE 201
||| : || :
DB 216 EQNEL-QNRLANVYSWIGLTQNGCP--WRWDGTDGFENGFRNMALPDQDNFGHGLGGGE 272
.:
OY 202 RCYYLNFKRSPEKRWGMNDVNLGPGORSYCEM 232
.:
DB 273 DCAHIT-TGCP-----WNDDVCQRTERFWICEM 298
.: :

RESULT 12
INMSER
I:IGE Fc receptor, low-affinity - mouse
N:Alternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte IGE receptor
C:Species: Mus musculus (house mouse)
C>Date: 12-Feb-1993 #sequence_revision 28-Oct-1994 #text-change 22-Jun-1999
C:Accession: A43518; A33840
R:Golindick, S.O.; Tronustine, M.L.; Yamashita, L.C.; Kehry, M.R.; Moore, K.W.
J. Immunol. 144, 1974-1982, 1990
A>Title: Isolation, characterization, and expression of cDNA clones encoding the mouse
A:Reference number: A43518; MUID:90171598; PMID:2137845
A:Accession: A43518
A:Molecule type: mRNA
A:Residues: 1-331 <GOI>
A:CROSS-references: GB:M4163; NID:g193242; PIDN:AA37603.1; PID:g309227
R:Bettler, B.; Hostetler, H.; Rao, M.; Yokoyama, W.M.; Kilcherr, F.; Conrad, D.H.
Proc. Natl. Acad. Sci. U.S.A. 86, 7566-7570, 1989
A>Title: Molecular structure and expression of the murine lymphocyte low-affinity receptor
A:Reference number: A33840; MUID:90017519; PMID:2529542
A:Accession: A33840
A:Molecule type: mRNA
A:Residues: 1-331 <BEH>
A:CROSS-references: GB:M99371; NID:g193245; PIDN:AA74898.1; PID:g193246; GB:M27150
C:Comment: This receptor for the Fc portion of IGE is expressed in various hematopoietic
f B-cells.
C:Superfamily: IGE receptor II; C-type lectin homology
F:1-35/Domain: intracellular #status predicted <INT>
F:14-22/Region: stop-transfer sequence
F:26-46/Domain: transmembrane #status predicted <EXT>
F:47-331/Domain: extracellular #status predicted <EXT>
F:66-86/Region: 21-residue repeat
F:87-107/Region: 21-residue repeat
F:108-128/Region: 21-residue repeat
F:129-149/Region: 21-residue repeat
F:186-305/Domain: C-type lectin homology <LCH>
F:65,114/Binding site: carbohydrate (asn) (covalent) #status predicted

```

Query Match Similarity    16.3%; Score 208.5; DB 1; Length 331;
Best Local Similarity     31.2%; Pred. No. 7.4e-11;
Matches      53; Conservative   34; Mismatches    60; Indels    23; Gaps    8;

OY      75 LLEKTKTELVTHTTECYVK---NMPEETAMSCCPKNMKSFSSNCYFISTESASWDS 130
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Cros    151 INERKTADSLEKLOEFAFKLMIELISKGTACNCPKNMLHFOQCKYCFGKSOMIOA 210
OY      131 EKDKARMHAHLIVINTOEODEPFIQNLOEBSAYFVGLSDPEGQRHMOWVDOTPTNESSTF 190
        |:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       211 RPACSDGLRVLVSHSQEDPLMQHINKKSW--IGLQDLNMEGEFVSDSPGYSN-- 267

OY      191 WHPREPSD--PNERCVLVNFRKSPKRMGMNVNCLGPQRS-----VCEMM 233
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       268 WNPGRPNNGGGEGDCVMN--RGSGQ---WNDAFC---RSYLDMAVCEQL 308

RESULT 13
2710
mouse receptor, macrophage - mouse
Alternate names: lambda lectin; phospholipase A2 receptor
C.Species: Mus musculus (house mouse)
C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
CAccession: T42710
R.Wu, K.; Yuan, J.; Tasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A.Title: Characterization of a novel member of the macrophage mannose receptor type C le
A.Reference number: T22235; MUID:96355501; PMID:8702911
A.Accession: T42710
A>Status: preliminary; translated from GB/EMBL/DBU
A.Molecule type: mRNA
A.Residues: 1-1479 <MAX>
A.Cross-references: EMBL:056734; NID:91336073; PID:91336074; PIDD:AAC52729.1
C.Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C.Keywords: membrane protein; receptor
F.186-227/Domain: fibronectin type II repeat homology <2Fr>

Query Match          16.2%; Score 207; DB 2; Length 1479;
Best Local Similarity 31.8%; Pred. No. 5.5e-10;
Matches      50; Conservative   27; Mismatches    54; Indels    26; Gaps    7;

OY      91 CVKKN----MPEETAMSC---CPKNMKSFSSNCYFISTESASMODESKCARMEAHIL 142
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       358 CKKRKNATVEIIPDRMTNVNAVECDPSMOPQGHCYRLQAKRRMSQEKRCCLAGGELL 417
OY      143 VINTOEODPIFQNL-QEBSAYEVGLSDPEGQRHMOWVDOTPTNESSTFWHPRPS---D 198
        |:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
        418 SIHSVAELFEFTIKQIQEVEELMWIGLNDLKQMNFWSDGSLV--SFTWHMPPEPPNRD 475

OY      199 PNERCVLVNFRKSPKRMG---NWMDNCLGPQRSCE 231
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       476 SLEDCTLT-----WGPEGRMWDSPCNOSLPISICK 504

RESULT 14
534198
IGE Fc receptor II, low-affinity - rat
N.Alternate names: CD23; lymphocyte IGE receptor
C.Species: Rattus norvegicus (Norway rat)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999
CAccession: S34198
R.Flores-Romo, L.; Shield, J.; Humbert, Y.; Graber, P.; Aubry, J.P.; Gauchat, J.F.; Ayala
submitted to the EMBL Data Library, June 1993
A.Description: Inhibition of an in vivo antigen-specific IGE response by antibodies to C
A.Reference number: S34198
A.Accession: S34198
A.Molecule type: mRNA
A.Residues: 1-309 <FLD>
A.Cross-references: EMBL:X73579; NID:9313672; PIDD:CAA51981.1; PID:9313673
C.Superfamily: IGE receptor II; C-type lectin homology
C.Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat; tr
F.14-22/Region: stop-transfer sequence

```

F:24-46/Domains: transmembrane #status predicted <TM>
F:47-309/Domains: extracellular #status predicted <EXT>
F:126-309/Product: soluble Ig9-binding factor (29K) #status predicted <IG1>
F:149-309/Product: soluble Ig9-binding factor (25-27K) #status predicted <BF1>
F:164-283/Domains: C-type lectin homology factor (IC9H)
F:192-283,260-274/Disulfide bonds: #status predicted

	Query Match	16.1%	Score 205.5	DB 1	Length 309
	Best Local Similarity	- 30.5%	Pred. No. 1.3e-10		
	Matches	53	Conservative	35	Mismatches 63; Indels 23; Gaps 8
QY	71	KYSOLLEKTKTKELVHTLLECVRK---	NMEVETAMSCCEPKNMKSFSFNSCYFIISTESAS	126	
Dd	125	KSQGLNEKRASDSLEKIQEEVAKLMILITLSMKGACNVCPDMLHFQOKCYFYFGSGSKQ	184		
QY	127	WQDEKCARNAHLVLINTQEEDFLIQNLQEEASATVYGLSDPEGCRHMQMVOTPIPNE	186		
Dd	185	WIOAKFTCSIDEGRLVSLHSQKEDFLMOQLINKESW--IGQDLIMDEGEFWPDSPGYV	243		
QY	187	SSTFMHPREPPD--PNERCYVLNFRKSPRKPMGVNDVNLGPORS-----VCDEM	233		
Dd	244	SN--WNAGEPLNNGGQGEDCVMM--RGSSQ---WMDAFC-----RSLIDMANVECOL	286		

RESULT 15
A46274
HIV gp120-binding C-type lectin - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995
C:Accession: A46274
R:Curulis, B.M.; Scharnowske, S.; Watson, A.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
A:Title: Sequence and expression of a membrane-associated C-type lectin that exhibits
A:Reference number: A46274; MUID:92390446; PMID:1518869
A:Accession: A46274
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-404 <CUR>
A:Experimental source: Placenta
A:Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIP:113135)
C:Superfamily: C-type lectin homology
C:256-377/Domain: C-type lectin homology <LCH>

[illegible]

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Search completed: August 4, 2003, 13:11:38
Job time : 41 secs
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Query Match Similarity 16.3%; Score 208.5; DB 1; Length 331;
Best Local Similarity 31.2%; Pred. No. 7.4e-11;
Matches 53; Conservative 34; Mismatches 60; Indels 23; Gaps 8;

OY 75 LLEKTKELVHTTIECVK---NMPVEETAMSCCPKNMKSFSSNCYFISTESASWDS 130
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Cros 151 INERKTADSLEKLOEFAVKLMIELISKGTACNICPKRWLHFOQCKCYFGKSOWIOA 210
OY 131 EKDKARMHAHLIVINTOEODEFIQNLOEBSAYFVGLSDPEGQRHMOWNVDOTPTNESSTF 190
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 211 RPACSDGLRVLVSHSQEDPLMQHIKKWSM-TGLQDLNMEGEFVSDSPVGYSN-- 267

OY 191 WHPREPSD-PNERCVYLNFRRKSPFKRMGMNVNCLGPQRS-----VCEMM 233
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 268 WNPGRPNNGGGGDCVMN-RGSQG---WNDAFC---RSVLDMAVCEQL 308

RESULT 13
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A.Accession: T42710
A>Status: preliminary; translated from GB/EMBL/DDBU
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A.Residues: 1-1479 <MAX>
A.Cross-references: EMBL:U56734; NID:91336073; PID:91336074; PIDD:AAC52729.1
C.Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C.Keywords: membrane protein; receptor
F.186-227/Domain: fibronectin type II repeat homology <2FR>

Query Match 16.2%; Score 207; DB 2; Length 1479;
Best Local Similarity 31.8%; Pred. No. 5.5e-10;
Matches 50; Conservative 27; Mismatches 54; Indels 26; Gaps 7;

OY 91 CVKKN----MPEVETAMSC---CPKNMKSFSSNCYFISTESASMODESKCARMEAHIL 142
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
Db 358 CKKRKNATVEDIOPDRMTNNVAVECDPSPQPGHCYRLQAKRSMQSEKRCCLAGGELL 417
    .|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
OY 143 VINTOEODFIFFQNL-QEBSAYEVGLSDPEGQRHMOWNVDOTPVNESSTFWHPRPS---D 198
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
    418 SIHSVAELEFTITKOKEVEBELMWIGLNDLKQMFMFSDGSLV-SFTWHHPPEPPNRD 475

OY 199 PNERCVYLNFRRKSPKRMG---NMWDNCLGPQRSCE 231
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
Db 476 SLEDCTLT-----WGPEGRMWDSPCNOSLPISICK 504

RESULT 14
534198
IGE Fc receptor II, low-affinity - rat
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C.Accession: S34198
R.Flores-Romo, L.; Shield, J.; Humbert, Y.; Graber, P.; Aubry, J.P.; Gauchat, J.F.; Ayala
submitted to the EMBL Data Library, June 1993
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A.Accession: S34198
A.Molecule type: mRNA
A.Residues: 1-309 <FLIO>
A.Cross-references: EMBL:X73579; NID:9313672; PIDD:CAA51981.1; PID:9313673
C.Superfamily: IGE receptor II; C-type lectin homology
C.Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat; tr
F.14-22/Region: stop-transfer sequence
```